

Yaen, Christopher

From: Yaen, Christopher
Sent: Tuesday, April 23, 2002 5:07 PM
To: STIC-Biotech/ChemLib
Subject: 09689469

could you please do a seq search on seq id no: 3-6 regular search (containing language) and oligo search (comprising language)

claims priority to 09/062,365 4/17/1998

thanks

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Patent Examiner
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CM1 6A04
703-308-3634

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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 8
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

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STN: _____
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Questel/Orbit: _____
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Lexis/Nexis: _____
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Other (specify): _____

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:41 ; Search time 66.52 seconds
(without alignments)
44.542 Million cell updates/sec

Title: US-09-689-469-3
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Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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20: /SID8/gcgdata/geneseq/AA1999.DAT:*

21: /SID8/gcgdata/geneseq/AA2000.DAT:*

22: /SID8/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	AA833191	Beta-amyloid pepti
2	40	100.0	40	AA860364	Beta-amyloid (1-40
3	40	100.0	40	AA837507	Amyloid beta prote
4	40	100.0	40	AA823335	Amyloid beta pepti
5	40	100.0	40	AA847226	Beta-amyloid pepti
6	40	100.0	40	AA839339	Beta-amyloid prote
7	40	100.0	40	AA839804	Beta-amyloid prote
8	40	100.0	40	AA825135	Human amyloid beta
9	40	100.0	40	AA814099	Human beta-amyloid
10	40	100.0	40	AA89584	Wild type aggregat
11	40	100.0	40	AA892723	Human tachykinin a

12	40	100.0	40	AA81473	Synthetic amyloid
13	40	100.0	40	AA805483	Human peptide anti
14	40	100.0	40	AA84426	Partial sequence o
15	40	100.0	40	AA891780	Amyloid beta-prote
16	40	100.0	40	AA891802	Amyloid beta-prote
17	40	100.0	40	AA891813	Amyloid beta-prote
18	40	100.0	40	AA891829	Amyloid beta-prote
19	40	100.0	41	AA860365	Beta-amyloid (1-41
20	40	100.0	41	AA825136	Human amyloid beta
21	40	100.0	41	AA811497	Human amyloid beta
22	40	100.0	42	AA820330	Sequence of A99 (b
23	40	100.0	42	AA860366	Beta-amyloid (1-42
24	40	100.0	42	AA895248	Beta/A4-amyloid pe
25	40	100.0	42	AA894591	Alzheimer amyloid
26	40	100.0	42	AA812828	Beta A4 peptide.
27	40	100.0	42	AA864507	Neurotoxic beta-am
28	40	100.0	42	AA847230	Beta-amyloid pepti
29	40	100.0	42	AA842389	Full length beta-a
30	40	100.0	42	AA849691	Human beta amyloid
31	40	100.0	42	AA833407	Human amyloidogeni
32	40	100.0	42	AA825137	Human amyloid beta
33	40	100.0	42	AA808607	Human beta-amyloid
34	40	100.0	42	AA829093	A-beta-binding pep
35	40	100.0	42	AA89585	Mutant aggregating
36	40	100.0	42	AA892726	Human tachykinin a
37	40	100.0	42	AA881474	Synthetic amyloid
38	40	100.0	42	AA86056	Beta-amyloid 1-42
39	40	100.0	42	AA882622	Amyloid-beta pepti
40	40	100.0	42	AA805484	Human peptide anti
41	40	100.0	42	AA886134	Human Alzheimer-be
42	40	100.0	42	AA891779	Amyloid beta-prote
43	40	100.0	42	AA891812	Amyloid beta-prote
44	40	100.0	42	AA849098	Human amyloid beta
45	40	100.0	42	AA848497	Human amyloid prot

ALIGNMENTS

RESULT	1
AA833191	AA833191 standard; peptide; 40 AA.
XX	
XX	AA833191;
XX	
XX	01-JUL-1993 (first entry)
XX	
XX	Beta-amyloid peptide.
XX	
XX	Alzheimer's disease; amyloid deposition; diagnosis; therapy.
XX	
XX	Synthetic.
XX	
XX	WO9304194-A.
XX	
XX	04-MAR-1993.
XX	
XX	
XX	10-AUG-1992; 92WO-US06700.
XX	
XX	
XX	13-AUG-1991; 91US-0744767.
XX	
XX	(HARD) HARVARD COLLEGE.
XX	(MINU) UNIV MINNESOTA.
XX	
XX	Maggio JE, Mantyh PW;
XX	
XX	WPI; 1993-094020/11.
XX	
XX	Detecting Alzheimer's disease using beta-amyloid peptide -
XX	includes quantitating amyloid deposition onto tissue samples, and
XX	using screen agents as therapeutic agents
XX	
XX	Disclosure; Page 34; 51pp; English.

XX The peptide is an internal fragment of the beta amyloid peptide (BAP)
 CC precursor, which was produced synthetically. The peptide, when
 CC labelled, may be used in in vitro methods for the detection of
 CC Alzheimer's disease.
 CC See also AAK33192.

SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 14; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
 Db 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40

RESULT 2

AA60364
 ID AAK60364 standard; peptide; 40 AA.

AC AAK60364;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-40).

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 KW anti-beta-amyloid antibody; diagnosis.

XX Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94MO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Kitada C, Odaka A, Suzuki N;

XX WPI; 1994-264110/32.

XX WPI; 1994-264110/32.

PT Antihodies recognising specific parts of beta-amyloid - can be

PT used for diagnosis of diseases implicating beta-amyloid, such as

PT Alzheimer's disease

XX Disclosure; Page 82; 116pp; Japanese.

XX Antihodies which recognise specific subfragments of the beta-amyloid

XX protein are claimed. Specifically, the antibodies (which are pref.

XX monoclinal) recognise residues 1-16 and/or 1-28 from the N-terminal

XX portion of beta-amyloid or they recognise residues 25-35 or 35-43

XX from the C-terminal portion. The antibodies are useful for assaying

XX beta-amyloid and its derivatives for diagnosis of Alzheimer's

XX disease.

SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 15; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Db 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40

RESULT 3

AAW37507
 ID AAW37507 standard; peptide; 40 AA.

AC AAW37507;

DT 20-APR-1998 (first entry)

DE Amyloid beta protein fragment (1-40) immunogen.

XX Amyloid beta protein; A beta; immunogen: human; Alzheimer's disease;

XX amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 16..17

XX EP783104-A1.

XX 09-JUL-1997.

XX 17-DEC-1996; 96EP-0120269.

XX 27-DEC-1995; 95JP-0351296.

XX (ORIG) ORIENTAL YEAST CO LTD.

XX Fujita T, Matuo Y, Taniguchi Y;

XX WPI; 1997-343989/32.

XX Assay for soluble amyloid precursor protein useful to diagnose

XX Alzheimer's disease - uses antibodies against amyloid beta-protein,

XX also new hybridoma producing antibodies

XX Example 1; Fig 2; 10pp; English.

XX A novel method has been developed of assaying for soluble amyloid

XX precursor protein (SAPP). The method uses an antibody against amyloid

XX beta-protein (A beta; produced from SAPP) or SAPP. The present sequence

XX represents amino acids 1 to 40 of amyloid beta-protein. SAPP can be

XX assayed accurately, and when including a monoclonal antibody recognising

XX the N-terminus of A beta and a monoclonal antibody recognising SAPP, the

XX assay can be used to diagnose Alzheimer's disease. Senior plaque

XX observed in the brain of Alzheimer's patients is primarily composed of

XX A beta, which is generated from SAPP. Simple and accurate assay of SAPP

XX is possible. The antibody (preferably monoclonal) preferably has an

XX antigen recognition site which is an amino acid sequence common to

XX A beta and SAPP, or specific to SAPP. The SAPP assayed for preferably

XX has part of the A beta sequence at its amino terminus and is preferably

XX solubilised through cleavage of the A beta between positions 16 (lysine)

XX and 17 (leucine) from the amino acid terminus. The preferred method

XX comprises immobilising one antibody (especially generated by (2)) on to

XX an insoluble carrier, capturing a substance to be assayed on to this

XX antibody, reacting another, labelling, antibody with the assay substance

XX and detecting the activity of the labelling substance bound to the

XX carrier.

SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 18; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

KW Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;
 KM cerebral blood vessel; sulphated macromolecule; Kuru;
 KM conophilic maltase-cross spherical amyloid plaque;
 KM Creutzfeldt-Jacob disease; Gertsman-Straussler syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO9945947-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 12-MAR-1999; 99WO-US05438.
 XX
 PR 13-MAR-1998; 98US-0077924.
 XX
 PA (UNITV) UNIV WASHINGTON.
 XX
 PI Castillo G, Snow AD;
 DR WPI; 1999-571686/48.
 XX
 PT Formation of amyloid plaques using amyloid protein and sulphated
 PT macromolecules; for, e.g. identification of agents for treating
 PT Alzheimer's disease -
 XX
 PS Claim 3; Page 87; 89pp; English.
 XX
 CC This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's
 CC disease is characterised by the accumulation of a 39-43 amino acid
 CC peptide termed the beta-amyloid peptide in the form of extracellular
 CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.
 CC The invention relates to methods for the formation of conophilic
 CC maltase-cross spherical amyloid plaques, which are characteristic of
 CC Alzheimer's disease. The amyloid plaques are formed by co-incubation of
 CC this beta-amyloid protein with sulphated macromolecules. The methods can
 CC be used to study the formation of amyloid plaques and to identify
 CC anti-plaque therapeutics. They can be used for diseases such as
 CC Alzheimer's disease, Creutzfeldt-Jacob disease, Gertsman-Straussler
 CC syndrome and Kuru.
 CC
 SQ Sequence 40 AA;
 XX
 XX
 Query Match 100.0%; Score 40; DB 20; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40
 XX
 RESULT 7
 AAY39804
 ID AAY39804 standard; peptide; 40 AA.
 XX
 AC AAY39804;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Beta-amyloid protein, Beta/A4 amyloid (1-40).
 XX
 KM Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KM long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KM multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; Kuru;
 KM carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KM endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KM Creutzfeldt-Jacob disease; Gertsman-Straussler Syndrome;
 KM subacute spongiform encephalopathy; therapy.
 XX
 OS Homo sapiens.
 OS
 PN US5958883-A.
 XX
 XX

XX
 PD 28-SEP-1999.
 XX
 PF 05-JUN-1995; 95US-0461216.
 XX
 PR 23-OCT-1992; 92US-0969734.
 XX
 PR 23-SEP-1992; 92US-0950417.
 XX
 PA (UNITV) UNIV WASHINGTON.
 XX
 PI Snow AD;
 DR WPI; 1999-561062/47.
 XX
 PT Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -
 XX
 PS Disclosure; Column 67-68; 83pp; English.
 XX
 CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jacob disease, Gertsman-Straussler Syndrome, Kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 CC
 SQ Sequence 40 AA;
 XX
 XX
 Query Match 100.0%; Score 40; DB 20; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40
 XX
 RESULT 8
 AAY25135
 ID AAY25135 standard; peptide; 40 AA.
 XX
 AC AAY25135;
 XX
 DT 26-AUG-1999 (first entry)
 XX
 DE Human amyloid beta-A4 peptide 2.
 XX
 KM Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KM therapeutic drug; brain; Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS
 PN US5919631-A.
 XX
 PD 06-JUL-1999.
 XX
 PF 17-JUL-1996; 96US-0682245.
 XX
 PR 17-JUL-1996; 96US-0682245.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 DR WPI; 1999-403957/34.
 XX
 XX


```

RESULT 11
AAW92723
ID AAW92723 standard; peptide; 40 AA.
XX
XX
AC AAW92723;
XX
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #69.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
XX Homo sapiens.
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Claim 1b; Column 41-42; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congenital angiodystrophy with cerebral
XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
XX
XX Sequence 40 AA;
XX
Query Match 100.0%; Score 40; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATIGLMVGCV 40
DB 1 daefrhdsgyevhhqklvfaedvgsnkgatiglmvgcv 40
RESULT 12
AAW81473
ID AAW81473 standard; peptide; 40 AA.
XX
XX
XX AAW81473;
XX
XX 28-JAN-1999 (first entry)
XX
XX Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
XX
XX Amyloid beta; Abeta; deoxygenerated solvent; evaporative deposition;
XX research; neurotoxicity; free-radical; glutamine synthetase.
XX

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OS Synthetic.
XX
XX US5840838-A.
XX
XX 24-NOV-1998.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX (KENT) UNIV KENTUCKY RES FOUND.
XX
XX Askenov M, Butterfield DA, Carney JM, Hensley K;
XX WPI; 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic
XX solvent treatment, useful for studying neurotoxicity
XX
XX Claim 5; Columns 11-12; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
XX peptides. The invention provides a process for treating a synthetic
XX Abeta peptide that comprises dissolving the peptide in a deoxygenerated
XX solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
XX sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
XX acetone to a concentration of 0.01-10 mg/mL. Incubating the
XX solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
XX 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta
XX peptides are useful as research tools for studying neurotoxicity
XX resulting from Abeta peptide -enhanced free-radical production. The
XX treatment increases the activity of the synthetic Abeta peptides in tests
XX to determine free-radical generating capacity and glutamine synthetase
XX inactivation.
XX
XX Sequence 40 AA;
XX
Query Match 100.0%; Score 40; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATIGLMVGCV 40
DB 1 daefrhdsgyevhhqklvfaedvgsnkgatiglmvgcv 40
RESULT 13
AAE05483
ID AAE05483 standard; peptide; 40 AA.
XX
XX
XX AAE05483;
XX
XX 24-SEP-2001 (first entry)
XX
XX Human peptide antigen comprising beta amyloid (Abeta) 40.
XX
XX Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive;
XX neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
XX age-related cognitive function loss; senile dementia; Wilson's disease;
XX Parkinson's disease; amyloidotic lateral sclerosis; cerebroprotective;
XX cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
XX Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
XX Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
XX myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
XX Gilles de la Tourette's syndrome; nocturnal; chronic seizure disorder;
XX brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
XX AIDS; dementia; alcoholism; autism; retinal ischemia; ophthalmological;
XX autonomic function disorder; Friedrich's ataxia; schizophrenia; therapy;
XX vasotropic; neuroprotective; anti-HIV; human immunodeficiency virus;
XX anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
XX Homo sapiens.
XX

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[illegible]

PR	08-DEC-1999;	99US-0169687.
XX		
PA	(MIND-) MINDSET BIOPHARMACEUTICALS USA INC.	
XX		
PI	Chain B;	
XX		
DR	WPI: 2001-381648/40.	
XX		
PT	Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to T cell epitope -	
PS	Claim 3; Page 41; 47pp; English.	
XX		
CC	The present sequence represents a partial sequence of a human beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a N- or C-terminal end-specific B cell epitope from a naturally occurring internal peptide cleavage product of a precursor or mature protein, as a free N- or C-terminus, joined to a T cell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betapP peptides slow down, reduce or prevent the accumulation of amyloid beta peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They also block the interaction of amyloid beta peptides with other molecules that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide cleavage product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal.	
CC	Sequence	40 AA;
SQ		
Query Match	100.0%;	Score 40; DB 22; Length 40;
Best Local Similarity	100.0%;	Pred. No. 5.8e-36;
Matches	40; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 DAEFRHDGSEVHHOKLVEFADVDGSNKGATIGLMGVV	40
Dd	1 daefrhdsgyevhnqklvfaedvgnsnkgaiglmgyvv	40
RESULT	15	
ID	AAB91780	
AC	AAB91780 standard; Peptide; 40 AA.	
XX		
DT	22-JUN-2001 (first entry)	
DE	Amyloid beta-protein fragment peptide SEQ ID NO:956.	
XX		
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyI; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.	
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO200069900-A2.	
PD	23-NOV-2000.	
PF	17-MAY-2000; 2000WO-US13576.	
XX		
PR	17-MAY-1999; 99US-0134406.	
PR	10-SEP-1999; 99US-0154306.	
PR	15-OCT-1999; 99US-0159783.	
XX		
PA	(CONU-) CONUTCHEM INC.	
XX		

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 XX

PS Disclosure; Page 506; 733pp: English.
 XX

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimido and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX

SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 22; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGEVYHQRKLVFPAEDVGSNKGAIIGLMVGVV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 daefrndsgyewhqbklvfaedvgsnkgailglmvgvv 40

Search completed: April 24, 2002, 09:21:50
 Job time: 249 sec

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 40
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 45

RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 40
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 45

RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 40
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 45

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 40
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 45

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 40
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGV 45

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MUID:93075180

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:11 ; Search time 38.65 seconds
(without alignments)
78.835 Million cell updates/sec

Title: US-09-689-469-3
Perfect score: 40
Sequence: 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	100.0	42	2	PN0512	beta-amyloid prote
2	40	100.0	57	2	E60045	Alzheimer's diseas
3	40	100.0	57	2	F60045	Alzheimer's diseas
4	40	100.0	57	2	G60045	Alzheimer's diseas
5	40	100.0	57	2	D60045	Alzheimer's diseas
6	40	100.0	57	2	A60045	Alzheimer's diseas
7	40	100.0	57	2	B60045	Alzheimer's diseas
8	40	100.0	82	2	PQ0438	Alzheimer's diseas
9	40	100.0	695	1	A47975	Alzheimer's diseas
10	40	100.0	770	1	QRH044	Alzheimer's diseas
11	27	67.5	695	2	A27485	Alzheimer's diseas
12	27	67.5	695	2	S00550	Alzheimer's diseas
13	17	42.5	747	2	JH0773	Alzheimer's diseas
14	15	37.5	33	2	S23094	beta-amyloid prote
15	15	37.5	247	2	B83880	3-oxoacyl-(acyl-ca
16	7	17.5	416	2	S16306	membrane protein P
17	7	17.5	416	2	B85558	probable transport
18	6	15.0	64	2	S10640	epua protein - Stri
19	6	15.0	122	2	S54715	probable aspartate
20	6	15.0	130	2	S63533	profilin basic iso
21	6	15.0	152	2	T06645	hypothetical prote
22	6	15.0	173	2	S44399	NADH dehydrogenase
23	6	15.0	176	2	B83837	hypothetical prote
24	6	15.0	182	2	T35807	hypothetical prote
25	6	15.0	184	1	A30128	synchronous muscul
26	6	15.0	189	2	H83281	conserved hypothet
27	6	15.0	190	2	G84182	hypothetical prote
28	6	15.0	192	2	T22142	hypothetical prote
29	6	15.0	205	2	F72422	KHG-KDPC b1func10

30	6	15.0	205	2	G82358	conserved hypothet
31	6	15.0	213	2	D86170	hypothetical prote
32	6	15.0	214	2	S39644	acetoin utilizatio
33	6	15.0	219	2	I52644	neuronal protein -
34	6	15.0	230	2	B82456	probable acetyltra
35	6	15.0	234	2	H85138	hypothetical prote
36	6	15.0	234	2	E70982	probable magnesium
37	6	15.0	266	2	T10609	hypothetical prote
38	6	15.0	273	2	T06661	hypothetical prote
39	6	15.0	284	2	S04723	genome polypeptid
40	6	15.0	289	2	E64330	dihydrodipicolinat
41	6	15.0	290	2	E86284	hypothetical prote
42	6	15.0	291	2	H81132	hypothetical prote
43	6	15.0	291	2	E81890	hypothetical prote
44	6	15.0	292	1	A39871	calponin alpha, sm
45	6	15.0	297	1	S31484	calponin H1 - pig

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamlya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A:Reference number: PN0512; MUID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHIT>
A:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 40; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40
DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 45

A:Accession: P00438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAY>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.9e-35;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHOKLVFAEDVGSNKGATIGLMVGCV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 17 DAEFRHDSGEVHOKLVFAEDVGSNKGATIGLMVGCV 56

RESULT 9
 A:Accession: A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 40; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 1.8e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHOKLVFAEDVGSNKGATIGLMVGCV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 597 DAEFRHDSGEVHOKLVFAEDVGSNKGATIGLMVGCV 636

RESULT 10
 ORHUA
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I39562; A44
 4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
 R:Lemaitre, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The Prec4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A>Note: alternative splice form APP(695)
 R:Lemaitre, H.G.

submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360
 A>Note: alternative splice form APP(695)
 R:La Faut, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <IAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA13654.1; PID:9516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865
 R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AAB59502.1; PID:9178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLMPVPAPEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AAB59501.1; PID:9178615
 R:Yoshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEPV>
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620
 A>Note: a mutation with 693-Gln is presented
 R:Wurrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I39562; MUID:92022553
 A:Accession: I39562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AAB19991.1; PID:9236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbom, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 araki, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:9257377; PIDN:AA823645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:9257379; PIDN:AA823646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115376)
 A:Note: This sequence has a silent mutation
 A:Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.; Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:9178539; PIDN:AA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.; Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid A
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:9178706; PIDN:AA53540.1; PID:g178707
 A:Experimental source: brain
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:9177957; PIDN:AA51564.1; PID:g177958
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 A:Residues: 672-678 <DYR>
 R:Tanai, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:g929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>

A:Cross-references: GB:X06989; EMBL:X00297; NID:928720; PIDN:CAA30050.1; PID:g28721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.; Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:g929611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AA51726.1; PID:g178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 40; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMGVV 40
 Db 672 DAEFRHDSGYEVHHOKLVFAEDVGSNKGATIGLMGVV 711
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text, change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.; Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AA537139.1; PID:g309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.; Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379
R:Rizumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: 149485; MUID:9220998
A:Accession: 149485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 67.5%; Score 27; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 9.4e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFADVGSNKGAITGLMWGVV 40
|||||
Db 610 HOKLVFADVGSNKGAITGLMWGVV 636

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:86312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SH1>
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA030488.1; PID:955617
R:Schubert, D.; Schroeder, R.; Lacombiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 67.5%; Score 27; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 9.4e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFADVGSNKGAITGLMWGVV 40
|||||
Db 610 HOKLVFADVGSNKGAITGLMWGVV 636

RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:9263150; PIDN:AA024853.1; PID:9263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.5%; Score 17; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 VGSNKGAITGLMWGVV 40
|||||
Db 672 VGSNKGAITGLMWGVV 688

RESULT 14
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
A:Reference number: S23094; MUID:92316198
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <ROJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 37.5%; Score 15; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFADVGSNK 28
|||||
Db 19 HOKLVFADVGSNK 33

RESULT 15
B83880
3-oxoacyl-(acyl-carrier protein) reductase B81842 [Imported] - Bacillus halodurans (S
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: B83880
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: B83880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <STO>

A:Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05561.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1842
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 17.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 KGAIIGL 34
|||||
DB 159 KGAIIGL 165

Search completed: April 24, 2002, 09:23:15
Job time: 244 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:21 ; Search time 32.21 seconds
(without alignments)
27.946 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 40
Sequence: 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGAVV 40

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	1	US-07-744-767A-1
2	40	100.0	40	1	US-08-235-400-2
3	40	100.0	40	1	US-08-476-464A-2
4	40	100.0	40	1	US-08-304-585-1
5	40	100.0	40	1	US-08-302-808-3
6	40	100.0	40	2	US-08-433-734-1
7	40	100.0	40	2	US-08-609-090-8
8	40	100.0	40	2	US-07-737-371E-69
9	40	100.0	40	2	US-08-682-245A-2
10	40	100.0	40	2	US-08-986-948-3
11	40	100.0	40	2	US-08-461-216-1
12	40	100.0	40	4	US-08-959-148-1
13	40	100.0	40	5	PCT-US92-06700-1
14	40	100.0	41	1	US-08-302-808-4
15	40	100.0	41	2	US-08-682-245A-3
16	40	100.0	41	2	US-08-986-948-4
17	40	100.0	42	1	US-07-744-767A-2
18	40	100.0	42	1	US-08-179-574-1
19	40	100.0	42	1	US-08-347-144-1
20	40	100.0	42	1	US-08-462-859A-19
21	40	100.0	42	1	US-08-123-659A-19
22	40	100.0	42	1	US-08-464-247A-19
23	40	100.0	42	1	US-08-464-248A-19
24	40	100.0	42	1	US-08-476-464A-1
25	40	100.0	42	1	US-08-304-585-2
26	40	100.0	42	1	US-08-302-808-5
27	40	100.0	42	1	US-08-268-348A-1

28	40	100.0	42	2	US-08-433-734-2	Sequence 2, Appl1
29	40	100.0	42	2	US-08-609-090-9	Sequence 9, Appl1
30	40	100.0	42	2	US-07-737-371E-72	Sequence 72, Appl1
31	40	100.0	42	2	US-08-422-333-4	Sequence 4, Appl1
32	40	100.0	42	2	US-08-682-245A-4	Sequence 4, Appl1
33	40	100.0	42	2	US-08-986-948-5	Sequence 5, Appl1
34	40	100.0	42	3	US-08-717-551A-2	Sequence 2, Appl1
35	40	100.0	42	4	US-09-388-890-1	Sequence 1, Appl1
36	40	100.0	42	4	US-09-005-215-20	Sequence 20, Appl1
37	40	100.0	42	5	PCT-US92-06700-2	Sequence 2, Appl1
38	40	100.0	42	5	PCT-US93-00325-1	Sequence 1, Appl1
39	40	100.0	43	1	US-08-235-400-1	Sequence 1, Appl1
40	40	100.0	43	1	US-08-437-067-1	Sequence 1, Appl1
41	40	100.0	43	1	US-08-302-808-6	Sequence 6, Appl1
42	40	100.0	43	1	US-08-079-511-1	Sequence 1, Appl1
43	40	100.0	43	1	US-08-467-607-1	Sequence 1, Appl1
44	40	100.0	43	2	US-08-404-831-1	Sequence 1, Appl1
45	40	100.0	43	3	US-08-976-179-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-744-767A-1
; Sequence 1, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantlyn, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-744-767A-1

Query Match 100.0%; Score 40; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGAVV 40
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Db 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGAVV 40

RESULT 2
US-08-235-400-2
Sequence 2, Application US/08235400
Patent No. 5552426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Moon, James A.
APPLICANT: Zimmerman, Dennis M.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TIME OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36, 808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-2

Query Match 100.0%; Score 40; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 3
US-08-476-464A-2
Sequence 2, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match 100.0%; Score 40; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 4
US-08-304-585-1
Sequence 1, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantlyn, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueitling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueitling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-304-585-1

Query Match 100.0%; Score 40; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40
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DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 5

US-08-302-808-3
; Sequence 3, Application US/08302808
; Patent No. 5750349

GENERAL INFORMATION:

APPLICANT: SUZUKI, No. 5750349uhlro

APPLICANT: ODAKA, Asano

APPLICANT: KITADA, Chieko

TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

DERIVATIVES AND USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02019

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,808

FILING DATE: 15-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00089

FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993

FILING DATE: 25-JAN-1993

APPLICATION NUMBER: 019035/1993

FILING DATE: 05-FEB-1993

APPLICATION NUMBER: 28685/1993

FILING DATE: 16-NOV-1993

APPLICATION NUMBER: 334773/1993

FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 44631

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-302-808-3

Query Match 100.0%; Score 40; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40
|||||
DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 6

US-08-433-734-1
; Sequence 1, Application US/08433734
; Patent No. 5837473

GENERAL INFORMATION:

APPLICANT: Magglio, John E.

APPLICANT: Mantyh, Patrick W.

TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods

FOR USE IN Detecting Alzheimer's Disease

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.

STREET: P.O. Box 581415

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55458-1415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/433,734

FILING DATE: 03-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muelting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110,00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1220

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-433-734-1

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40
|||||
DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 7

US-08-609-090-8
; Sequence 8, Application US/08609090
; Patent No. 5840838

GENERAL INFORMATION:

APPLICANT: HENSLEY, Kenneth

APPLICANT: BUTTERFIELD, D. A.

APPLICANT: CARNEY, John M.

APPLICANT: AKSENOV, Michael

TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KRAUS, ERIC J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-8

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40

RESULT 8
US-07-737-371E-69
Sequence 69, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CLASSIFICATION: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO.: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-69

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40

RESULT 9
US-08-682-245A-2
Sequence 2, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHERPAL
APPLICANT: PAUL, JOSEPH W.
APPLICANT: RIEDEL, NORBERT G.
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-2

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40
DB 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 10
US-08-986-948-3
; Sequence 3, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317unhito
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 0101332/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-3

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40

DB 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 11
US-08-461-216-1
; Sequence 1, Application US/08461216
; Patent No. 5958883
; GENERAL INFORMATION:
; APPLICANT: SNOW, A. D.
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOEW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: (SYMBOL 98 \f "Symbol")/A4(1-40);
; DESCRIPTION: FIGURES 23-29
US-08-461-216-1

Query Match 100.0%; Score 40; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40
DB 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAITGLMWGVV 40

RESULT 12
US-08-959-148-1
; Sequence 1, Application US/08959148
; Patent No. 6172277
; GENERAL INFORMATION:
; APPLICANT: Tate, Barbara A.
; APPLICANT: Majoie, Ronald
; APPLICANT: Neaton, Julie L.
; TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
; FILE REFERENCE: 04930/022001
; CURRENT APPLICATION NUMBER: US/08/959,148

;; CURRENT FILING DATE: 1997-10-28
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 1
;; LENGTH: 40
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-959-148-1

Query Match 100.0%; Score 40; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 13

PCT-US92-06700-1
; Sequence 1, Application PC/TUS9206700
; GENERAL INFORMATION:
; APPLICANT: Mantyh, Patrick W.
; APPLICANT: Magglo, John E.
; TITLE OF INVENTION: Labelled -Amyloid Peptide
; TITLE OF INVENTION: and Alzheimer's Disease Detection
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 Northwest Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
; COMPUTER: Northgate 386
; OPERATING SYSTEM: DOS 4.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06700
; FILING DATE: 19920810
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalczyk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.226-WO-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 332-5300
; TELEFAX: (612) 332-9081
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Internal fragment of the -
; NAME/KEY: amyloid peptide precursor
; LOCATION: Sequence of 40 amino acid residues
; LOCATION: the -amyloid peptide precursor
PCT-US92-06700-1

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Query Match 100.0%; Score 40; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 14

US-08-302-808-4
; Sequence 4, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302, 808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 SPRE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-4

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
Query Match 100.0%; Score 40; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 15
US-08-682-245A-3
Sequence 3, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SHAHSAABDHE, SODHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BAA PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-3

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Query Match	100.0%	Score 40;	DB 2;	Length 41;
Best Local Similarity	100.0%	Pred. No. 1,9e-34;		
Matches 40;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DAEFRHDSGYEYHHOKLVEFAEDVGSNKGATIGLVGGYV	40	
Db	1	DAEFRHDSGYEYHHOKLVEFAEDVGSNKGATIGLVGGYV	40	

Search completed: April 24, 2002, 09:22:29
Job time: 248 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:47 ; Search time 21.46 Seconds

(without alignments)
68.341 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 40

Sequence: 1 DAEFRHDSGYEVHOKLVEFAEDVGSNKGATIGLVAGVY 40

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 3664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	57	A4_PIG	Q29023 sus scrofa
2	40	100.0	57	A4_URMA	Q29149 ursus marit
3	40	100.0	58	A4_CANFA	Q28280 canis fami1
4	40	100.0	58	A4_RABIT	Q28748 oryctolagus
5	40	100.0	58	A4_SHEEP	Q28757 ov1s aries
6	40	100.0	59	A4_BOVIN	Q28053 bos taurus
7	40	100.0	751	A4_SATSC	Q95241_salmi1r1 sci
8	40	100.0	770	A4_HUMAN	P05067 homo sapien
9	27	67.5	770	A4_MOUSE	P18023 mus musculu
10	27	67.5	770	A4_RAT	P24077 escherichia
11	17.5	416	1	VADA_ECOLI	Q24077 escherichia
12	7	17.5	546	UBIB_SALTY	Q916m4 salmone11a
13	6	15.0	64	EPVA_STRPN	Q03159 streptococc
14	6	15.0	130	PROF_ENTHI	P43230 cephalospor
15	6	15.0	173	NT6M_CEPCC	P43197 cephalospor
16	6	15.0	184	MP20_DROME	P14318 drosophila
17	6	15.0	199	NP25_MOUSE	O91198 mus musculu
18	6	15.0	213	AAT_STRGR	P36692 streptomyc
19	6	15.0	214	ACUB_BACSU	P33066 bacillus su
20	6	15.0	219	NP25_RAT	P37805 rattus norv
21	6	15.0	262	FLGG_RHIME	O52946 rhizobium m
22	6	15.0	282	NP25_HUMAN	O94115 homo sapien
23	6	15.0	284	POLG_PVYTO	P11897 potato viru
24	6	15.0	287	LEP4_LEGN	O61433 legionella
25	6	15.0	289	DAPA_METJA	O57695 methanococc
26	6	15.0	292	CLPO_CHICK	P26932 gallus gall
27	6	15.0	297	CLP1_HUMAN	P51911 homo sapien
28	6	15.0	297	CLP1_MOUSE	O08091 mus musculu
29	6	15.0	297	CLP1_PIG	O08092 sus scrofa
30	6	15.0	297	CLP1_RAT	O08092 sus scrofa
31	6	15.0	321	CYE_GUTTH	O78494 guillardia
32	6	15.0	321	EUM1_EURMA	P25780 eurogi1yphus
33	6	15.0	321	PUR_MOUSE	P42669 mus musculu

34	6	15.0	322	1	PUR_HUMAN	O00577 homo sapien
35	6	15.0	327	1	POLG_PVYCH	P21294 potato viru
36	6	15.0	330	1	COPR_PEMV	P07993 pepper moti
37	6	15.0	339	1	IC11_TRIHA	P34053 trichoderma
38	6	15.0	387	1	CTRB_NEIMB	P32014 neisseria m
39	6	15.0	391	1	CPSD_STRAG	O04664 streptococc
40	6	15.0	397	1	AAT_STRAG	O60013 streptomyc
41	6	15.0	405	1	GSPE_PSEAE	O00513 pseudomonas
42	6	15.0	428	1	CPYL_PSEBP	P33006 pseudomonas
43	6	15.0	429	1	AROA_CORGL	O92470 corynebacte
44	6	15.0	442	1	CEM1_YEAST	P39525 saccharomyc
45	6	15.0	450	1	AROA_MYCTU	P22487 mycobacteri

ALIGNMENTS

RESULT	ID	STANDARD	PRT	57 AA
1	A4_PIG			
AC	Q29023:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID			
DE	PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).			
GN	APP.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Brain;			
RX	MEDLINE=92017079; PubMed=1656157;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid			
RT	peptide in dog, polar bear and five other mammals by cross-species			
RL	polymerase chain reaction analysis."			
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).			
CC	- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO			
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN			
CC	G(O) (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: X56127; GAA39592.1; -			
DR	HSSP: P05067; IAML.			
DR	InterPro: IPR001688; A4_APP.			
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.			
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.			
FT	NON_TER	1		
FT	CHAIN	6	48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	<1	33	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	34	57	POTENTIAL.
FT	NON_TER	57		
SO	SEQUENCE	57 AA; 6172 MW; 84209D88BBA82DFA CRC64;		

Query Match 100.0%; Score 40; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHOKLVEFAEDVGSNKGATIGLVAGVY 40

Db 6 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIIGLMVGCV 45

RESULT 2

A4_URSMA STANDARD; PRT; 57 AA.

ID A4_URSMA

Q29149;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OC Ursus maritimus (Polar bear) (Thalarchos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=9615;

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: X56128; CAA39593.1; -.

DR HSSP: P05067; IAML.

DR Interpro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT NON_TER

FT SEQUENCE

57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match

Best Local Similarity 100.0%; Score 40; DB 1; Length 57;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIIGLMVGCV 40

Db 6 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIIGLMVGCV 45

RESULT 3

A4_CANFA STANDARD; PRT; 58 AA.

ID A4_CANFA

Q28280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

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DR EMBL: X56125; CAA39590.1; -.

DR HSSP: P05067; IAML.

DR Interpro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT NON_TER

FT SEQUENCE

58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match

Best Local Similarity 100.0%; Score 40; DB 1; Length 58;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIIGLMVGCV 40

Db 7 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIIGLMVGCV 46

RESULT 4

A4_RABIT STANDARD; PRT; 58 AA.

ID A4_RABIT

Q28748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RL	Brain Res. Mol. Brain Res. 10:299-305(1991).	
CC	-I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO	
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN	
CC	G(O) (BY SIMILARITY).	
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-I- SIMILARITY: BELONGS TO THE APP FAMILY.	
CC	-----	
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CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; X56129; CAA39594.1; .	
DR	HSSP; P05067; IAML.	
DR	InterPro; IPR001868; A4_APP.	
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.	
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.	
KW	Glycoprotein; Amyloid; Neutrone; Transmembrane.	
FT	NON_TER	1
FT	CHAIN	6
FT	DOMAIN	48
FT	DOMAIN	<1
FT	TRANSMEM	33
FT	DOMAIN	57
FT	NON_TER	58
FT	NON_TER	58
SO	SEQUENCE	58 AA; 6300 MW; F434209D88BBA82D CRC64;
		BETA-AMYLOID PROTEIN (POTENTIAL).
		EXTRACELLULAR (POTENTIAL).
		POTENTIAL.
		CYTOPLASMIC (POTENTIAL).

```

Query Match 100.0%: Score 40; DB 1; Length 58;
Best Local Similarity 100.0%: Pred. No. 1,2e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAILGMVGCV 40
      |||
Db      6 DAEFRHDSGYEVHHOKLVFEADVGSNKGAILGMVGCV 45
      |||

RESULT      5
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-ApP) (A-BETA)] (FRAGMENT).
GN App.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -! FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -! SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC
CC
DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; 1AML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutroic; Transmembrane.
FT NON_TER 1
FT CHAIN 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 33 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 34 57 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SO SEQUENCE 58 AA; 6300 MW; F434209D86BBA2D CRC64;

```

Query Match          100.0%; Score 40; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. NO. 1.2e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGEYVHHOKLVFFADVYSNKGATIGLVGCV 40
        |||||||
Db      6 DAEFRHDSGEYVHHOKLVFFADVYSNKGATIGLVGCV 45

RESULT 6
A4_BOVIN STANDARD: PRT: 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
DE APP.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RX MEDLINE=92017079; PubMed=1656157;
RC TISSUE=Brain;
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X56124; CAA39589.1; -
DR EMBL, X56126; CAA39591.1; -
DR HSSP, P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

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FT  NON_TER      1      1
FT  CHAIN         7      49
FT  DOMAIN        <1     34
FT  TRANSMEM      35     58
FT  DOMAIN        59     59
FT  NON_TER       59     59
SQ  SEQUENCE      59 AA; 6414 MW; F43469DA88A2E12D CRC64;

Query Match      100.0%; Score 40; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIIGLMGVGV 40
    |||||||||||||||||||||||||||||||||||
DB  7 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIIGLMGVGV 46

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC  095241;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
    AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP.
OS  Saimiri sciureus (Common squirrel monkey).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX  NCBI_TaxID=9521;
RN  [1];
RP  TISSUE=Liver, and kidney;
RC  MEDLINE=96108492; PubMed=8532114;
RA  Levy E., Amorim A., Frangione B., Walker L.C.;
RT  "Beta-amyloid precursor protein gene in squirrel monkeys with
    cerebral amyloid angiopathy.";
RL  Neurobiol. Aging 16:805-808(1995).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
    INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
    G(O).
CC  -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC  -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
    WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
    RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
    NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
    PHOSPHORYLATION (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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    or send an email to license@sib-sib.ch).
CC  -----
CC  EMBL: S81024; AADI4347.1; -
CC  InterPro: IPR001868; A4_APP.
CC  InterPro: IPR002223; Kunitz_BPTI.
CC  Pfam: PF02177; A4_EXTRA; 1.
CC  Pfam: PF00014; Kunitz_BPTI; 1.
CC  PRINTS: PR00203; AMYLOIDA4.
CC  PRINTS: PR00204; BETAAMYLOID.
CC  PRINTS: PR00759; BASICPTASE.
CC  SMART: SM00006; A4_EXTRA; 1.
CC  SMART: SM00131; KU; 1.
CC  PROSITE: PS00319; A4_EXTRA; 1.
CC  PROSITE: PS00320; A4_INTRA; 1.
CC  PROSITE: PS00280; BPTI_KUNITZ_1; 1.

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DR  PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM  Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW  Signal; Serine protease inhibitor.
FT  SIGNAL        1      17
FT  CHAIN         18     751
FT  DOMAIN        653     695
FT  TRANSMEM      18     680
FT  TRANSMEM      681     704
FT  DOMAIN        705     751
FT  DOMAIN        287     345
FT  SITE          740     743
FT  ACT_SITE      301     302
FT  DISULFID      291     341
FT  DISULFID      300     324
FT  DISULFID      316     337
FT  CARBOHYD      523     523
FT  CARBOHYD      552     552
SQ  SEQUENCE      751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match      100.0%; Score 40; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 9.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIIGLMGVGV 40
    |||||||||||||||||||||||||||||||||||
DB  653 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIIGLMGVGV 692

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
AC  P05067; P09000; Q16011;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
    (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP OR A4 OR CVAP OR ADL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1];
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=87144572; PubMed=2881207;
RA  Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RT  Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT  "The precursor of Alzheimer's disease amyloid A4 protein resembles a
    cell-surface receptor.";
RL  Nature 325:733-736(1987).
RN  [2];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=88122639; PubMed=2893289;
RA  Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RT  Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA  Cordell B.;
RT  "A new A4 amyloid mRNA contains a domain homologous to serine
    proteinase inhibitors.";
RL  Nature 331:525-527(1988).
RN  [3];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89128427; PubMed=2783775;
RA  Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RT  Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT  "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
    is encoded by 16 exons.";
RL  Nucleic Acids Res. 17:517-522(1989).
RN  [4];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97263807; PubMed=9108164;
RA  Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,

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RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus."; *Nucleic Acids Res.* 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lampert I.D., Villa-Komaroff L.,
 RA Gsell J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease."; *Nature* 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity."; *Nature* 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex."; *Proc. Natl. Acad. Sci. U.S.A.* 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tountouloute W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels."; *J. Neurochem.* 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshitaka S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene."; *Gene* 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mila S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide."; *Nucleic Acids Res.* 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts."; *J. Biol. Chem.* 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor."; *Biochem. Biophys. Res. Commun.* 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)"; *Nature* 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=9215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein."; *Nat. Struct. Biol.* 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor."; *Biochemistry* 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamarcik M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein."; *Biochemistry* 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marchowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide."; *Biochemistry* 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment."; *Biochemistry* 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
 RT environment. Is the membrane-spanning domain where we think it is?"; *Biochemistry* 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site."; *J. Struct. Biol.* 130:142-152(2000).
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;

RA Dykx T., Weidemann A., Multhaupt G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RN EMBO J. 7:949-957(1988).
 RN [24]
 RP REVIEW.
 RP MEDLINE=92271194; PubMed=1589757;
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective.";
 RL Science 256:780-783(1992).
 RN [25]
 Query Match 100.0%; Score 40; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.8e-34;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 672 DAEFRHDSGYEYVHOKLVFAEDVGSNKGAIIGLMVGVV 40
 QY 1 DAEFRHDSGYEYVHOKLVFAEDVGSNKGAIIGLMVGVV 40
 DB 672 DAEFRHDSGYEYVHOKLVFAEDVGSNKGAIIGLMVGVV 711
 RESULT 9
 A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Bergh H.;
 RT "The amyloid beta protein precursor or protease nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RN Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domestica.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikaki S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS, APP(395), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X59379; ? NOT_ANNOTATED_CDS.
 DR EMBL: M18373; AAA37139.1; -;
 DR EMBL: X15210; CAA33280.1; -;
 DR EMBL: D10603; BAA01436.1; -;
 DR EMBL: M24397; AAA39929.1; -;
 DR PIR: A27485; A27485.
 DR PIR: S04855; S04855.
 DR PIR: S19727; S19727.
 DR MGI: 88059; App.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PRO0203; AMYLOIDA4.
 DR PRINTS: PRO0204; BETAMAMLOID.
 DR PRINTS: PRO0759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 770
 FT CHAIN 18 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT CARBOHYD 289 289
 FT VARSPIC 290 364
 FT VARSPIC 346 380
 FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;
 SO

Query Match 67.5%; Score 27; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVEFAEDVGSNKGAIIGLMVGVV 40
 |||||
 DB 685 HOKLVEFAEDVGSNKGAIIGLMVGVV 711

RESULT 10
 A4_RAT STANDARD: PRT: 770 AA.

AC P08592:
 DT 01-AUG-1988 (rel. 08, Created)
 DT 01-DEC-1992 (rel. 24, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDGENIC GLYCOPROTEIN) (AG).
 GN App.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X07648; CAA30488.1; -
 DR EMBL: X14066; CAA32229.1; -
 DR PIR: S00550; S00550.
 DR PIR: S03607; S03607.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00204; BETAMYLOID.
 DR PRINTS: PR00759; BASICPASE.
 DR SMART: SM00006; A4_EXTRA; 1.

DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT CARBOHYD 289 289
 FT VARSPLIC 290 364
 FT VARSPLIC 770 AA; 86704 MW; C26C9D6BBD29A7 CRC64;
 SQ SEQUENCE

Query Match 67.5%; Score 27; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVEFAEDVGSNKGAIIGLMVGVV 40
 |||||
 DB 685 HOKLVEFAEDVGSNKGAIIGLMVGVV 711

RESULT 11
 YBDA_ECOLI STANDARD: PRT: 416 AA.

ID YBDA_ECOLI
 AC P24077;
 DT 01-MAR-1992 (rel. 21, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE HYPOTHETICAL MEMBRANE PROTEIN P43.
 GN YBDA OR B0591.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92157868; PubMed=1838574;
 RA Shea C.M., McIntosh M.A.;
 RT "Nucleotide sequence and genetic organization of the ferric
 RT enterobactin transport system: homology to other periplasmic binding
 RT protein-dependent systems in Escherichia coli.";
 RL Mol. Microbiol. 5:1415-1428(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92157867; PubMed=1787794;
 RA Chenaunt S.S., Earhart C.F.;
 RT "Organization of genes encoding membrane proteins of the Escherichia
 RT coli ferriterobactin permease.";
 RL Mol. Microbiol. 5:1405-1413(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [41]
 RP SEQUENCE FROM N.A.
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 RA Federspiel N., Hyman R., Kalman S., Komp C., Kuri O., Lew H., Lin D.,
 RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -----
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 CC -----
 CC DR EMBL: X57470; CAA40706.1; -
 CC DR EMBL: X59402; CAA42044.1; -
 CC DR EMBL: AE000164; AAC73692.1; -
 CC DR EMBL: U82598; AAB40790.1; -
 CC DR PIR: S16295; S16295.
 CC DR PIR: S16306; S16306.
 CC DR PIR: S14850; S14850.
 CC DR Ecogene: EG11104; Ybda.
 CC KM Hypothetical protein: Transmembrane: Complete proteome.
 CC FT TRANSMEM 22 42 POTENTIAL.
 CC FT TRANSMEM 36 76 POTENTIAL.
 CC FT TRANSMEM 96 116 POTENTIAL.
 CC FT TRANSMEM 119 139 POTENTIAL.
 CC FT TRANSMEM 157 177 POTENTIAL.
 CC FT TRANSMEM 179 199 POTENTIAL.
 CC FT TRANSMEM 219 239 POTENTIAL.
 CC FT TRANSMEM 257 277 POTENTIAL.
 CC FT TRANSMEM 301 321 POTENTIAL.
 CC FT TRANSMEM 357 377 POTENTIAL.
 CC FT TRANSMEM 379 399 POTENTIAL.
 CC FT CONFLICT 123 123 F -> S (IN REF. 1).
 CC SQ SEQUENCE 416 AA; 43282 MW; 64FC9FAF99AC25A CRC64;
 QY 33 GLMVGCV 39
 DB 68 GLMVGCV 74
 ID UBIB_SALTY STANDARD: PRT; 546 AA.
 AC Q9L6M4;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROBABLE UBIQUITONE BIOSYNTHESIS PROTEIN UBIB.
 GN UBIB OR AARF OR STMD1.17.
 OS Salmonella typhimurium.
 CC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Salmonella.
 CC NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGGC1412;
 RA Waterston R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED, PROBABLY INDIRECTLY, FOR THE HYDROXYLATION OF
 CC 2-OCTAPRENYLPHENOL TO 2-OCTAPRENYL-6-HYDROXY-PHENOL, THE FOURTH
 CC STEP IN UBIQUINONE BIOSYNTHESIS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ABCI FAMILY. UBIB SUBFAMILY.

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 CC -----
 CC DR EMBL: AF233324; AAF34420.1; -
 CC DR Sylene; SG77777; ubib.
 CC KW Ubiquinone biosynthesis.
 CC SQ SEQUENCE 546 AA; 63238 MW; 362873022A808F1A CRC64;
 QY 34 LMVGCV 40
 DB 530 LMVGCV 536
 ID EPUA_STRPN STANDARD: PRT; 64 AA.
 AC Q03159;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE EPUA PROTEIN.
 GN EPUA.
 OS Streptococcus pneumoniae
 CC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC OC Streptococcus.
 CC NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=470;
 RC MEDLINE=90294291; PubMed=2359120;
 RA Puyet A., Greenberg B., Lacks S.A.;
 RT "Genetic and structural characterization of end. A membrane-bound
 RT nuclease required for transformation of Streptococcus pneumoniae.";
 RL J. Mol. Biol. 213:727-738(1990).
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 CC -----
 CC DR EMBL: X54225; CAA38133.1; -
 CC DR PIR: S10640; S10640.
 CC SQ SEQUENCE 64 AA; 7037 MW; DE5727DA7B5EBB92 CRC64;
 QY 32 IGLMVG 37
 DB 30 IGLMVG 35
 ID PROF_ENTHI STANDARD: PRT; 130 AA.
 AC P49230;
 DT 01-FEB-1996 (Rel. 33, Created)
 QY 32 IGLMVG 37
 DB 30 IGLMVG 35
 ID PROF_ENTHI STANDARD: PRT; 130 AA.
 AC P49230;
 DT 01-FEB-1996 (Rel. 33, Created)

```

DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-DEC-1998 (Rel. 37, last annotation update)
DE PROFILIN.
OS Entamoeba histolytica.
CC Eukaryota: Entamoebidae: Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 74-84 AND 86-94.
RC STRAIN=SF-3;
RX MEDLINE=96085166; PubMed=8521867;
RA Binder M., Ortner S., Erben H., Scheiner O., Wiedermann G.,
  Valenta R., Ducheine M.;
RT "The basic isoform of profilin in pathogenic Entamoeba histolytica.
  cDNA cloning, heterologous expression, and actin-binding
  properties."
RL Eur. J. Biochem. 233:976-981(1995).
CC -!- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE
  CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE
  POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW
  CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
  IP3 AND DG.
CC -!- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC
  ACTIN IN A 1:1 RATIO.
CC -!- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X90911; CAA62418.1; -.
DR HSPD: P07274; 1YPR.
DR InterPro: IPR002097; Profilin.
DR Pfam: PF00235; Profilin; 1.
DR SMART: SM00392; PROF; 1.
DR PROSITE: PS00414; PROFILIN; 1.
KW Actin-binding; Cytoskeleton.
SQ SEQUENCE 130 AA; 13237 MW; AFS0A8E08FA00A6F CRC64;

Query Match 15.0%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 GAIIGL 34
    |||||
Db 20 GAIIGL 25

RESULT 15
NO6M_CEPKO STANDARD: PRT; 173 AA.
AC P43197;
DT 01-NOV-1995 (Rel. 32, created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 15-JUL-1998 (Rel. 36, last annotation update)
DE MADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).
MT MTND6 OR ND6 OR NADH6.
OS Cepphus columba (Pigeon guillemot).
CC Mitochondrion.
CC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
CC Archosauia: Aves: Neognathae: Charadriiformes: Alcidae; Cepphus.
OX NCBI_TaxID=28696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363783; PubMed=8082208;
RA Moun T., Willassen N.P., Johansen S.;
RT "Intragenic rearrangements in the mitochondrial MADH dehydrogenase
  subunit 6 gene of vertebrates."
RL Curr. Genet. 25:554-557(1994).

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CC -!- CATALYTIC ACTIVITY: MADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X73918; CAA52123.1; -.
DR InterPro: IPR001457; Oxidored_q3.
DR Pfam: PF00499; oxidored_q3; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 173 AA; 17982 MW; AAAP84636E040DF8 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 LMWGV 39
    |||||
Db 98 LMWGV 103

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Search completed: April 24, 2002, 09:24:53
 Job time: 246 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:16 ; Search time 63.44 Seconds
(without alignments)
92.227 Million cell updates/sec

Title: US-09-689-469-3
Perfect score: 40
Sequence: 1 DAEFRDSCYEYHKKLVFAEDVGSNKGAITGLMYGVV 40

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_17.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	82	4 P78438	P78438 homo sapien
2	40	100.0	82	4 O16014	O16014 homo sapien
3	40	100.0	82	4 O16019	O16019 homo sapien
4	40	100.0	82	4 O16020	O16020 homo sapien
5	40	100.0	534	13 O93296	O93296 gallus gall
6	40	100.0	569	11 O9PVL1	O9PVL1 gallus gall
7	40	100.0	695	11 O60496	O60496 cavia porce
8	40	100.0	695	13 O9DGJ8	O9DGJ8 gallus gall
9	40	100.0	751	13 O9DCJ7	O9DCJ7 gallus gall
10	40	100.0	770	6 O9TUI0	O9TUI0 sus scrofa
11	38	95.0	97	4 O13778	O13778 homo sapien
12	33	82.5	33	4 O9UC33	O9UC33 homo sapien
13	31	77.5	780	13 O73683	O73683 tetraodon f
14	30	75.0	30	4 O9UC49	O9UC49 homo sapien
15	27	67.5	28	4 O9UCD1	O9UCD1 homo sapien
16	27	67.5	79	11 O35463	O35463 cricetus
17	27	67.5	607	11 O99K32	O99K32 mus musculu
18	27	67.5	695	11 P97487	P97487 mus musculu
19	23	57.5	49	6 O97917	O97917 bos taurus

20	19	47.5	19	4 O9UC8	O9UC8 homo sapien
21	18	45.0	699	13 O57394	O57394 narke japon
22	18	45.0	737	13 O93279	O93279 fugu rubrip
23	17	42.5	693	13 O98S60	O98S60 xenopus lae
24	17	42.5	695	13 O98SF9	O98SF9 xenopus lae
25	17	42.5	747	13 O91963	O91963 xenopus lae
26	15	37.5	612	13 O919E7	O919E7 brachydanio
27	11	27.5	20	4 O9UCB6	O9UCB6 homo sapien
28	7	17.5	247	2 O9KBT2	O9KBT2 bacillus ha
29	7	17.5	375	2 O66290	O66290 agrobacteri
30	7	17.5	528	2 O9A4N9	O9A4N9 caulobacter
31	7	17.5	546	2 O9L6M4	O9L6M4 salmonella
32	7	17.5	828	10 O9FGR1	O9FGR1 arabidopsis
33	6	15.0	119	6 O9GMM2	O9GMM2 sus scrofa
34	6	15.0	123	2 O53951	O53951 streptomyce
35	6	15.0	130	6 O29364	O29364 sus scrofa
36	6	15.0	131	5 O24897	O24897 echinococcu
37	6	15.0	138	12 O91Z07	O91Z07 potato viru
38	6	15.0	143	11 O9D6K2	O9D6K2 mus musculu
39	6	15.0	144	2 O9AM08	O9AM08 plectonema
40	6	15.0	152	10 O9STZ9	O9STZ9 arabidopsis
41	6	15.0	155	8 O79079	O79079 fatelconus
42	6	15.0	157	10 O9C5F3	O9C5F3 arabidopsis
43	6	15.0	170	8 O9MLH7	O9MLH7 paragonimus
44	6	15.0	175	5 O9VZ11	O9VZ11 drosophila
45	6	15.0	176	2 O9KCS1	O9KCS1 bacillus ha

ALIGNMENTS

RESULT	ID	Accession	Length	Score	Description
1	P78438	PRELIMINARY;	PRT;	82 AA.	
2	P78438	01-MAY-1997 (TRENBLREL. 03, Created)			
3	P78438	01-MAY-1997 (TRENBLREL. 03, last sequence update)			
4	P78438	01-MAR-2001 (TRENBLREL. 16, last annotation update)			
5	P78438	AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).			
6	P78438	APP.			
7	P78438	Os Homo sapiens (Human).			
8	P78438	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
9	P78438	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
10	P78438	NCBI_TaxID=9606;			
11	P78438	SEQUENCE FROM N.A.			
12	P78438	MEDLINE=89392030; PubMed=2675837;			
13	P78438	Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,			
14	P78438	Little S.P.;			
15	P78438	"Alzheimer's disease amyloid peptide is encoded by two exons and shows			
16	P78438	similarity to soybean trypsin inhibitor.";			
17	P78438	Biochem. Biophys. Res. Commun. 163:1248-1255(1989).			
18	P78438	[2]			
19	P78438	SEQUENCE OF 19-48 FROM N.A.			
20	P78438	MEDLINE=87120329; PubMed=2949367;			
21	P78438	Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,			
22	P78438	Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neyer R.L.;			
23	P78438	"Amyloid beta protein gene: cDNA, mRNA distribution, and genetic			
24	P78438	linkage near the Alzheimer locus.";			
25	P78438	Science 235:880-884(1987).			
26	P78438	[3]			
27	P78438	SEQUENCE OF 32-63 FROM N.A.			
28	P78438	MEDLINE=93035397; PubMed=1415269;			
29	P78438	Kamino K., Orr H.T., Payami H., Wajzman E.M., Alonso M.E., Pulst S.M.,			
30	P78438	Anderson L., O'dahl S., Nemens E., White J.A.;			
31	P78438	"Linkage and mutational analysis of familial Alzheimer disease			
32	P78438	kindreds for the APP gene region.";			
33	P78438	Am. J. Hum. Genet. 51:998-1014(1992).			
34	P78438	EMBL: M29270; AA51768.1;			
35	P78438	EMBL: M29269; AA51768.1;			
36	P78438	EMBL: M15532; AA51768.1;			
37	P78438	EMBL: S45136; AAB3646.1;			
38	P78438	HSSP; P05067; 1BA4.			

FT NON_TER 1 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40
DB 17 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 56

RESULT 2

ID 016014 PRELIMINARY; PRT: 82 AA.

AC 016014; 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)
GN BETA-AMYLROID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; AAB26263.2; -

DR HSSP; P05067; IBA4.
FT NON_TER 1 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 3

ID 016019 PRELIMINARY; PRT: 82 AA.

AC 016019; 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)
GN BETA-AMYLROID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61380; AAB26264.2; -

DR HSSP; P05067; IBA4.
FT NON_TER 1 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 4

ID 016020 PRELIMINARY; PRT: 82 AA.

AC 016020; 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)
GN BETA-AMYLROID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61383; AAB26265.2; -

DR HSSP; P05067; IBA4.
FT NON_TER 1 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5B5D9230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 5

ID 093296 PRELIMINARY; PRT: 534 AA.

AC 093296; 01-NOV-1998 (TREMBLREL. 08, Created)
DT 01-NOV-1998 (TREMBLREL. 08, last sequence update)
DE 01-JUN-2001 (TREMBLREL. 17, last annotation update)
GN AMYLROID PRECURSOR PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RT "Increased production of amyloid precursor protein provides a
substrate for Caspase 3 in dying motoneurons.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF042098; AAC25052.1; -

DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLROIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;
Query Match
Best Local Similarity 100.0%; Score 40; DB 13; Length 534;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 436 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 475
RESULT 6
Q9PVL1 PRELIMINARY; PRT; 569 AA.
ID Q9PVL1
AC Q9PVL1
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.D., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;
Query Match
Best Local Similarity 100.0%; Score 40; DB 13; Length 569;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 472 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 511
RESULT 7
Q060496 PRELIMINARY; PRT; 695 AA.
ID Q060496
AC Q060496
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Beck M., Mueller D., Bigl V.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
DR EMBL: X97631; CA66230.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match
Best Local Similarity 100.0%; Score 40; DB 11; Length 695;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 597 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 636
RESULT 8
Q9DGJ8 PRELIMINARY; PRT; 695 AA.
ID Q9DGJ8
AC Q9DGJ8
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOROM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAG00593.1; -.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;
Query Match
Best Local Similarity 100.0%; Score 40; DB 13; Length 695;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40
DB 597 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 636
RESULT 9
Q9DGJ7 PRELIMINARY; PRT; 751 AA.
ID Q9DGJ7
AC Q9DGJ7
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOROM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RA Sarraa M., Rodolose A., Sorribas V.;
RT "cloning of full-length chicken beta-amyloid precursor protein
isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AF289219; AAG00594.1; -.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E7BE9413A8033D84 CRC64;

QY Query Match 100.0%; Score 40; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 653 DAERHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 40
1 DAERHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 692

RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AB032550; BAA84580.1; -.
DR HSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS50280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

QY Query Match 100.0%; Score 40; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAERHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 40

Db 672 DAERHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 711
1 DAERHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 711

RESULT 11
Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldhaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL: M15533; AAA35540.1; -.
DR HSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA.
FT NON_TER 1 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

QY Query Match 95.0%; Score 38; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EFRHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 38
3 EFRHDSGYEVHHOKLVFAEDVGSNKGALIGLMVGCV 40

RESULT 12
Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
biological fluids.";
RL Nature 359:325-327(1992).
DR HSP: P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DFE2FA167ABD0 CRC64;

QY Query Match 82.5%; Score 33; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAERHDSGYEVHHOKLVFAEDVGSNKGALIG 33
1 DAERHDSGYEVHHOKLVFAEDVGSNKGALIG 33

RESULT	13			
073683		PRELIMINARY;	PTM;	780 AA.
ID	073683			
AC	073683;			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, last annotation update)		
DE	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS:			
DE	BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].			
GN	APP.			
OS	Tetracodon fluviatilis (Puffer fish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	Tetraodontidae; Tetraodon.			
OX	NCBI_TaxID=47145;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9852138; PubMed=959080;			
RA	Villard L., Tassone F., Cnognorac-Jurcevic T., Clancy K., Gardiner K.,			
RT	"Analysis of pufferfish homologues of the A4-rich human APP gene.";			
RL	Gene 210:17-74(1998).			
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO			
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN			
CC	(G/O) (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION			
CC	WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC			
CC	RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE			
CC	NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF			
CC	PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-1- SIMILARITY: CONTAINS AN INHIBITOR DOMAIN BELONGING TO THE			
CC	BPT1/KUNITZ FAMILY OF INHIBITORS.			
DR	EMBL; AF018165; AAC41275.1; -			
DR	HSSP; P05067; 10CM.			
DR	InterPro; IPR001868; A4_APP.			
DR	InterPro; IPR002223; Kunitz_BPT1.			
DR	Pfam; PF02177; A4_EXTRA; 1.			
DR	Pfam; PF00014; Kunitz_BPT1; 1.			
DR	PRINTS; PR00203; AMYLOIDA4.			
DR	PRINTS; PR00759; BASICPASE.			
DR	SMART; SM0006; A4_EXTRA; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00319; A4_EXTRA; 1.			
DR	PROSITE; PS00320; A4_INTRA; 1.			
DR	PROSITE; PS00280; BPT1_KUNITZ_1; FALSE_NEG.			
DR	PROSITE; PS50279; BPT1_KUNITZ_2; 1.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;			
KW	Serine protease inhibitor.			
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	780	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT	FT			HOMOLOG.
FT	CHAIN	682	724	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	19	711	EXTRACELLULAR (POTENTIAL).
FT	TRANSELM	712	732	POTENTIAL.
FT	DOMAIN	733	780	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	323	382	BPT1/KUNITZ INHIBITOR.
FT	SITE	769	772	CLATHRIN-BINDING (BY SIMILARITY).
FT	DISULFD	327	378	BY SIMILARITY.
FT	DISULFD	336	361	BY SIMILARITY.
FT	CARBOHD	560	560	N-LINKED (GLCNAC..)
SO	SEQUENCE	780 AA;	88238 MW;	60071BE9452019D CRC64; (POTENTIAL).

```

RESULT      14
Q9UCG9      PRELIMINARY; PRT; 30 AA.
AC          Q9UCG9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RL Alzheimer's disease patient."
DR Ann. Neurol. 35:245-246(1994).
HSSP: P05067: 1BA4.
SO SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match
Best Local Similarity 75.0%; Score 30; DB 4; Length 30;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKA 30
    |||||||
Db 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKA 30

RESULT      15
Q9UCD1      PRELIMINARY; PRT; 28 AA.
ID          Q9UCD1;
AC          Q9UCD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vigo-Pellfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RL fluid."
DR J. Neurochem. 61:1965-1968(1993).
HSSP: P05067: 1AMB.
SO SEQUENCE 28 AA; 3244 MW; DE7BD081160AFc81 CRC64;

Query Match
Best Local Similarity 67.5%; Score 27; DB 4; Length 28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVNHOKLVFAEDVGSN 27
    |||||||
Db 1 DAEFRHDSGYEVNHOKLVFAEDVGSN 27

```


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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:15:16 ; Search time 66.28 Seconds
(without alignments)
44.703 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEHVHOKLVFAEDVGNKGAITGLMGVV 40

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT:*
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6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT:*
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18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT:*
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21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	40	AA833191	Beta-amyloid pepti
2	209	100.0	40	AA860364	Beta-amyloid (1-40
3	209	100.0	40	AAW3507	Amyloid beta prote
4	209	100.0	40	AAW23335	Amyloid beta pepti
5	209	100.0	40	AAW47226	Beta-amyloid pepti
6	209	100.0	40	AAW39339	Beta-amyloid prote
7	209	100.0	40	AAW39804	Beta-amyloid prote
8	209	100.0	40	AAW25135	Human amyloid beta
9	209	100.0	40	AAW14099	Human beta-amyloid
10	209	100.0	40	AAW9584	Wild type aggregat
11	209	100.0	40	AAW92723	Human tachykinin a

12	209	100.0	40	AAW81473	Synthetic amyloid
13	209	100.0	40	AAE05483	Human peptide anti
14	209	100.0	40	AAW84426	Partial sequence o
15	209	100.0	40	AAW91780	Amyloid beta-prote
16	209	100.0	40	AAW91802	Amyloid beta-prote
17	209	100.0	40	AAW91813	Amyloid beta-prote
18	209	100.0	40	AAW91829	Amyloid beta-prote
19	209	100.0	41	AAW60365	Beta-amyloid (1-41
20	209	100.0	41	AAW25136	Human amyloid beta
21	209	100.0	41	AAW11497	Human amyloid beta
22	209	100.0	42	AAW20330	Sequence of A99 (b
23	209	100.0	42	AAW60366	Beta-amyloid (1-42
24	209	100.0	42	AAW95248	Beta/A4-amyloid pe
25	209	100.0	42	AAW94591	Alzheimer amyloid
26	209	100.0	42	AAW12828	Beta A4 peptide.
27	209	100.0	42	AAW64507	Neurotoxic beta-am
28	209	100.0	42	AAW47230	Beta-amyloid pepti
29	209	100.0	42	AAW42989	Full length beta-a
30	209	100.0	42	AAW49691	Human beta amyloid
31	209	100.0	42	AAW33407	Human amyloidogen
32	209	100.0	42	AAW25137	Human amyloid beta
33	209	100.0	42	AAW08607	Human beta-amyloid
34	209	100.0	42	AAW25093	A-beta-binding pep
35	209	100.0	42	AAW9585	Mutant aggregating
36	209	100.0	42	AAW92726	Human tachykinin a
37	209	100.0	42	AAW81474	Synthetic amyloid
38	209	100.0	42	AAW96956	Beta-amyloid 1-42
39	209	100.0	42	AAW82622	Amyloid-beta pepti
40	209	100.0	42	AAE05484	Human peptide anti
41	209	100.0	42	AAW86134	Human Alzheimer be
42	209	100.0	42	AAW91779	Amyloid beta-prote
43	209	100.0	42	AAW91812	Amyloid beta-prote
44	209	100.0	42	AAW49098	Human amyloid beta
45	209	100.0	42	AAW48497	Human amyloid prot

ALIGNMENTS

RESULT 1
ID AAR33191 standard; peptide: 40 AA.
XX
AC AAR33191;
XX
DT 01-JUL-1993 (first entry)
XX
DE Beta-amyloid peptide.
XX
KW Alzheimer's disease; amyloid deposition; diagnosis; therapy.
XX
OS Synthetic.
XX
PN WO9304194-A.
XX
PD 04-MAR-1993.
XX
PF 10-AUG-1992; 92WO-US06700.
XX
PR 13-AUG-1991; 91US-0744767.
XX
PA (HARD) HARVARD COLLEGE.
PA (MING) UNIV MINNESOTA.
XX
Maggio JE, Mantyh PW;
XX
DR WPI, 1993-094020/11.
XX
PT Detecting Alzheimer's disease using beta-amyloid peptide -
PT includes quantitating amyloid deposition onto tissue samples, and
XX using screen agents as therapeutic agents
XX
PS Disclosure: Page 34; 51pp; English.

XX The peptide is an internal fragment of the beta amyloid peptide (BAP)
 CC precursor, which was produced synthetically. The peptide, when
 CC labelled, may be used in in vitro methods for the detection of
 CC Alzheimer's disease.
 CC See also AAR3192.

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 14; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40
 DB 1 daefrhdsgyevhhoklvffaedvgsnkgaiiglmvgvv 40

RESULT 2

AAR60364
 ID AAR60364 standard; peptide; 40 AA.

AC AAR60364;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-40).

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 KW anti-beta-amyloid antibody; diagnosis.

OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94MO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kitada C, Odaka A, Suzuki N;

XX WPI: 1994-264110/32.

XX PT Antibodies recognising specific parts of beta-amyloid - can be
 PT used for diagnosis of diseases implicating beta-amyloid, such as
 PT Alzheimer's disease

XX PS disclosure; Page 82; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
 CC from the C-terminal portion. The antibodies are useful for assaying
 CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
 CC disease.

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 15; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

DB 1 daefrhdsgyevhhoklvffaedvgsnkgaiiglmvgvv 40

RESULT 3

AAM37507
 ID AAM37507 standard; peptide; 40 AA.

AC AAM37507;

DT 20-APR-1998 (first entry)

DE Amyloid beta protein fragment (1-40) immunogen.

XX Amyloid beta protein; A beta; immunogen; human; Alzheimer's disease;
 KW amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

PN Cleavage-site 16..17

PN EP783104-A1.

PD 09-JUL-1997.

PF 17-DEC-1996; 96EP-0120269.

PR 27-DEC-1995; 95JP-0351296.

XX (ORIT) ORIENTAL YEAST CO LTD.

XX Fujita T, Matuo Y, Taniguchi Y;

XX WPI: 1997-343989/32.

XX PT Assay for soluble amyloid precursor protein useful to diagnose
 PT Alzheimer's disease - uses antibodies against amyloid beta-protein,
 PT also new hydridoma producing antibodies

XX PS Example 1; Fig 2; 10pp; English.

XX A novel method has been developed of assaying for soluble amyloid
 CC precursor protein (SAPP). The method uses an antibody against amyloid
 CC beta-protein (A beta), produced from SAPP or SAPP. The present sequence
 CC represents amino acids 1 to 40 of amyloid beta-protein. SAPP can be
 CC assayed accurately, and when including a monoclonal antibody recognising
 CC the N-terminus of A beta and a monoclonal antibody recognising SAPP, the
 CC assay can be used to diagnose Alzheimer's disease. Senior plaque
 CC observed in the brain of Alzheimer's patients is primarily composed of
 CC A beta, which is generated from SAPP. Simple and accurate assay of SAPP
 CC is possible. The antibody (preferably monoclonal) preferably has an
 CC antigen recognition site which is an amino acid sequence common to
 CC A beta and SAPP, or specific to SAPP. The SAPP assayed for preferably
 CC has part of the A beta sequence at its amino terminus and is preferably
 CC solubilised through cleavage of the A beta between positions 16 (lysine)
 CC and 17 (leucine) from the amino acid terminus. The preferred method
 CC comprises immobilising one antibody (especially generated by (2)) on to
 CC an insoluble carrier, capturing a substance to be assayed on to this
 CC antibody, reacting another, labelling, antibody with the assay substance
 CC and detecting the activity of the labelling substance bound to the
 CC carrier.

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 18; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

DB 1 daefrhdsgyevhbkqlvffaedvgsnkgaiiglmvgvv 40

RESULT 4

ID AAW23335 standard; peptide; 40 AA.

AC AAW23335;

DT 12-MAR-1998 (first entry)

DE Amyloid beta peptide 1 used to inhibit damage to cells in Alzheimer's.

KM Amyloid beta peptide; extracellular deposit; Alzheimer's disease;

KW neurite outgrowth; microglial activation; neuronal cell degeneration;

KM amyloid beta peptide fibril.

OS Homo sapiens.

PN WO9726913-A1.

PD 31-JUL-1997.

PF 21-JAN-1997; 97WO-US00857.

PR 26-JAN-1996; 96US-0592070.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D, Yan SD;

DR WPI; 1997-393374/36.

PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an

PS agent which inhibits interaction of an amyloid-beta peptide with a

CC Peptides AAW23335-36 are portions of the the amyloid beta peptide, which

CC is the principal component of extracellular deposits in Alzheimer's

CC disease. It has been shown to promote neurite outgrowth, generate

CC reactive oxygen intermediates, induce cellular oxidant stress, lead to

CC neuronal cytotoxicity, and promote microglial activation. The present

CC peptide, which comprises amino acids 1-40 of the amyloid beta peptide,

CC is used in a pharmaceutical composition. This composition comprises an

CC agent capable of inhibiting interaction of an amyloid-beta peptide with

CC a receptor for advanced glycosylation and product and a carrier. A

CC method for inhibiting interaction of amyloid beta peptide with a receptor

CC for advanced glycosylation on the surface of a cell comprises contacting

CC the cell with e.g. present peptide. Depending on the type of cell,

CC inhibiting the interaction between the amyloid beta peptide and the

CC receptor for advanced glycosylation can be used for inhibiting

CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta

CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid

CC beta peptide into a fibril, inhibiting aggregation of amyloid beta

CC peptide on the surface of a cell, inhibiting infiltration of a microglial

DB 1 daefrhdsgyevhbkqlvffaedvgsnkgaiiglmvgvv 40

RESULT 5

ID AAW47226 standard; peptide; 40 AA.

AC AAW47226;

DT 22-MAY-1998 (first entry)

DE Beta-amyloid peptide residues 1-40.

KM Screening assay; beta-amyloid peptide; treatment;

KW amyloidosis disease; Alzheimer's disease.

OS Homo sapiens.

PN US5721106-A.

PD 24-FEB-1998.

PF 12-SEP-1994; 94US-0304585.

PR 12-SEP-1994; 94US-0304585.

PA 13-AUG-1991; 91US-0744767.

PA (HARD) HARVARD COLLEGE.

PI (MINU) UNIV MINNESOTA.

DR WPI; 1998-168404/15.

PT New in vitro screening assay for Alzheimer's disease drugs -

PS comprises assessing binding of labelled beta-amyloid peptide to silk

CC Claim 8; Columns 29-30; 36pp; English.

CC The present sequence was used in the development of a novel in

CC vitro screening assay for agents capable of affecting the

CC deposition of beta-amyloid peptide (BAP) on tissue. The method

CC comprises contacting a silk sample with labelled BAP, optionally

CC in the presence of a test agent, detecting the amount of label

CC bound to the silk and assessing the effect of the agent on the

CC deposition of BAP. Agents that inhibit binding of BAP to silk are

CC potentially useful for treating amyloidosis diseases, especially

CC Alzheimer's disease.

CC

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CC

CC

DB 1 daefrhdsgyevhbkqlvffaedvgsnkgaiiglmvgvv 40

RESULT 6

ID AAY39339 standard; protein; 40 AA.

AC AAY39339;

DT 01-DEC-1999 (first entry)

DE Beta-amyloid protein.

KM Screening assay; beta-amyloid peptide; treatment;

KW amyloidosis disease; Alzheimer's disease.

OS Homo sapiens.

PN US5721106-A.

PD 24-FEB-1998.

PF 12-SEP-1994; 94US-0304585.

PR 12-SEP-1994; 94US-0304585.

PA 13-AUG-1991; 91US-0744767.

PA (HARD) HARVARD COLLEGE.

PI (MINU) UNIV MINNESOTA.

DR WPI; 1998-168404/15.

PT New in vitro screening assay for Alzheimer's disease drugs -

PS comprises assessing binding of labelled beta-amyloid peptide to silk

CC Claim 8; Columns 29-30; 36pp; English.

CC The present sequence was used in the development of a novel in

CC vitro screening assay for agents capable of affecting the

CC deposition of beta-amyloid peptide (BAP) on tissue. The method

CC comprises contacting a silk sample with labelled BAP, optionally

CC in the presence of a test agent, detecting the amount of label

CC bound to the silk and assessing the effect of the agent on the

CC deposition of BAP. Agents that inhibit binding of BAP to silk are

CC potentially useful for treating amyloidosis diseases, especially

CC Alzheimer's disease.

CC

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CC

KM Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;
 KM cerebral blood vessel; sulphated macromolecule; kuru;
 KM conophilic maltase-cross spherical amyloid plaque;
 KM Creutzfeldt-Jacob disease; Gertmann-Straussler syndrome.
 OS Homo sapiens.
 PN W09945947-A1.
 XX 16-SEP-1999.
 XX 12-MAR-1999: 99WO-US05438.
 XX 13-MAR-1998: 98US-0077924.
 XX (UNIV) UNIV WASHINGTON.
 PA Castillo G, Snow AD;
 PI WPI; 1999-571666/48.
 DR
 XX
 XX Formation of amyloid plaques using amyloid protein and sulphated
 PT macromolecules for, e.g. identification of agents for treating
 PT Alzheimer's disease
 XX
 XX Claim 3; Page 87; 89pp; English.
 PS
 XX This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's
 CC disease is characterised by the accumulation of a 39-43 amino acid
 CC peptide termed the beta-amyloid peptide in the form of extracellular
 CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.
 CC The invention relates to methods for the formation of conophilic
 CC maltase-cross spherical amyloid plaques, which are characteristic of
 CC Alzheimer's disease. The amyloid plaques are formed by co-incubation of
 CC this beta-amyloid protein with sulphated macromolecules. The methods can
 CC be used to study the formation of amyloid plaques and to identify
 CC anti-plaque therapeutics. They can be used for diseases such as
 CC Alzheimer's disease, Creutzfeldt-Jacob disease, Gertmann-Straussler
 CC syndrome and kuru.
 CC
 SO Sequence 40 AA;
 XX
 XX
 Query Match 100.0%; Score 209; DB 20; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGCEVHHOKIVFFAEDVGSNKGAITGLMGVV 40
 DB 1 daefrhdsgcevhqhkvlfadvgnsnkgaigtlmvgvv 40
 RESULT 7
 AAY39804
 ID AAY39804 standard; peptide; 40 AA.
 AC AAY39804;
 XX
 XX 29-NOV-1999 (first entry)
 DT
 XX
 XX Beta-amyloid protein, Beta/A4 amyloid (1-40).
 DE
 XX
 XX Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KM long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KM multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
 KM carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KM endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KM Creutzfeldt-Jacob disease; Gertmann Straussler Syndrome;
 KM subacute spongiform encephalopathy; therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 PN US5958863-A.

XX
 PD 28-SEP-1999.
 XX
 PF 05-JUN-1995: 95US-0461216.
 XX
 XX 23-OCT-1992: 92US-0969734.
 PR 23-SEP-1992: 92US-0950417.
 XX
 XX (UNIV) UNIV WASHINGTON.
 PA
 XX
 XX Snow AD;
 PI
 XX
 XX WPI; 1999-561062/47.
 DR
 XX
 XX Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -
 PT
 XX
 PS Disclosure; Column 67-68; 83pp; English.
 XX
 XX This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jacob disease, Gertmann Straussler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 CC
 SO Sequence 40 AA;
 XX
 XX
 Query Match 100.0%; Score 209; DB 20; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGCEVHHOKIVFFAEDVGSNKGAITGLMGVV 40
 DB 1 daefrhdsgcevhqhkvlfadvgnsnkgaigtlmvgvv 40
 RESULT 8
 AAY25135
 ID AAY25135 standard; peptide; 40 AA.
 AC AAY25135;
 XX
 XX 26-AUG-1999 (first entry)
 DT
 XX
 XX Human amyloid beta-A4 peptide 2.
 DE
 XX
 XX Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;
 KM therapeutic drug; brain; Alzheimer's disease.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 PN US5919631-A.
 PD
 XX
 XX 06-JUL-1999.
 XX
 PF 17-JUL-1996: 96US-0682245.
 PR 17-JUL-1996: 96US-0682245.
 XX
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 PA
 XX
 XX Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 PI
 XX
 XX WPI; 1999-403957/34.
 DR
 XX

PT Determination of degree of aggregation of a peptide, useful for
XX identifying therapeutic drugs for treating Alzheimer's disease
XX
PS Disclosure; Column 5-6; 8pp; English.
XX
CC This invention describes a novel method for the determination of the
CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.
CC Determination comprises: (a) incubating a sample of unaggregated
CC (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to
CC unaggregated (I); (b) measuring the amount of (II) bound to (I) to
CC obtain a value (I); (c) repeating steps (a) and (b) with a second
CC sample at a different time to obtain a second value (II); and (d)
CC determining the difference between (I) and (II) which is inversely
CC related to the degree of aggregation of (I). This method may be
CC applied to a screen for compounds that inhibit aggregation of (I).
CC These inhibitors may be used as therapeutic drugs to inhibit the
CC formation of these aggregates in the brains of patients suffering
CC from Alzheimer's disease.
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFADVGSNKGAIIGLMVGVV 40
DB 1 daefrhdsgyevhbkvlvfaedvgsnkgallglmvgvv 40

RESULT 9
ID AAY14099 standard; peptide; 40 AA.
XX AAY14099;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human beta-amyloid protein fragment.
XX
KW Beta-amyloid; human; amyloid plaque deposition; Alzheimer's disease;
KW induction; AD; sleep; circadian activity; circadian rhythm disturbance.
XX
OS Homo sapiens.
XX
PN WO9921978-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98MO-US22731.
XX
PR 28-OCT-1997; 97US-0959148.
XX
PA (MIRI-) MIRIAM HOSPITAL LIFESPAN PARTNER.
XX
PI Majocha R, Newton JL, Tate BA;
XX
DR WPI, 1999-326700/27.
XX
PT Inducing amyloid plaque deposition in a mammal, used to screen for
PT agents against Alzheimer's disease
XX
PS Claim 2; Page 30; 43pp; English.
XX
CC This sequence represents a fragment of the human beta-amyloid protein,
CC and can be used in the method of the invention. The method is for
CC inducing amyloid plaque deposition in a mammal by infusing into the brain
CC an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque
CC deposition has been induced are models of human Alzheimer's disease (AD)
CC and are used to screen for agents (A) that inhibit: (a) deposition of
CC amyloid plaque; and (b) AD-associated disruptions to sleep and circadian
CC activity. They may also be used to study the etiology of AD. Compared

CC with known methods for inducing plaque deposition, this process causes
CC less mechanical damage; the vehicle used is less neurotoxic and at basic
CC pH (I) is soluble enough for delivery by continuous infusion with
CC effective delivery to brain tissue. The control peptide causes few, if
CC any, plaques and does not stimulate an immune response. Most (I)-treated
CC animals develop AD-type pathology (contrast transgenic models of the
CC disease), including sleep and circadian rhythm disturbances.
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFADVGSNKGAIIGLMVGVV 40
DB 1 daefrhdsgyevhbkvlvfaedvgsnkgallglmvgvv 40

RESULT 10
ID AAM99584 standard; peptide; 40 AA.
XX AAM99584;
XX
DT 22-JUN-1999 (first entry)
XX
DE Wild type aggregating amyloid-beta peptide.
XX
KW Aggregation; amyloid-beta peptide; fluorescent group; detection;
KW diagnosis; Alzheimer's disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9908695-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98MO-US16809.
XX
PR 14-AUG-1997; 97US-0055660.
XX
PA (REGC) UNITV CALIFORNIA.
XX
PI Garzon-Rodriguez W, Glabe C;
XX
DR WPI, 1999-190112/16.
XX
PT New fluorescent labeled amyloid A-beta peptides
XX
PS Example 1; Page 21; 50pp; English.
XX
CC This sequence corresponds to an aggregating amyloid-beta peptide which
CC can be covalently labelled with a fluorescent group. The detection or
CC monitoring of an amyloid aggregate in a sample can be used to diagnose
CC or detect a predisposition to Alzheimer's disease. The screening assays
CC can be used to identify compounds for the treatment or amelioration of
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
CC amyloid-beta peptide are also useful for exploring other aspects of the
CC amyloid structure.
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFADVGSNKGAIIGLMVGVV 40
DB 1 daefrhdsgyevhbkvlvfaedvgsnkgallglmvgvv 40

```

RESULT 11
ID AAW92723 standard; peptide; 40 AA.
XX
XX AAW92723;
AC
XX
XX 30-APR-1999 (first entry)
DE Human tachykinin agonist beta-amyloid peptide fragment #69.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
PN US5876948-A.
PD 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
PI
XX WPI: 1999-189630/16.
DR
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PS Claim 1b; Column 41-42; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 40 AA;

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```

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DAEFRHDSGEYEHQKLVFEADVGSKNGAIIIGLWGVV 40
   |||||||||||||||||||||||||||||||||||
DB 1 daefrhdsgyevhqbklvfaedvgnskgaillglwgvv 40

```

```

RESULT 12
ID AAW81473 standard; peptide; 40 AA.
XX
XX AAW81473;
AC
XX
XX 28-JAN-1999 (first entry)
DE Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
XX
XX Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
XX

```

```

OS Synthetic.
XX
XX US5840838-A.
PN
XX
XX 24-NOV-1998.
PD
XX
XX 29-FEB-1996; 96US-0609090.
PF
XX
XX 29-FEB-1996; 96US-0609090.
PR
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
PA
XX
XX Aksekov M, Butterfield DA, Carney JM, Hensley K;
PI
XX WPI: 1999-034120/03.
DR
XX
XX Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
PS Claim 5; Columns 11-12; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC "evaporative deposition" in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
SQ Sequence 40 AA;

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```

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DAEFRHDSGEYEHQKLVFEADVGSKNGAIIIGLWGVV 40
   |||||||||||||||||||||||||||||||||||
DB 1 daefrhdsgyevhqbklvfaedvgnskgaillglwgvv 40

```

```

RESULT 13
ID AAE05483 standard; peptide; 40 AA.
XX
XX AAE05483;
AC
XX
XX 24-SEP-2001 (first entry)
DE Human peptide antigen comprising beta amyloid (Abeta) 40.
XX
XX Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive;
KW neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
KW age-related cognitive function loss; senile dementia; Wilson's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;
KW cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
KW Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
KW Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
KW myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
KW Gilles de la Tourette's syndrome; nocturnal; chronic seizure disorder;
KW brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
KW AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological;
KW autonomic function disorder; Friedreich's ataxia; schizophrenia; therapy;
KW vasotrophic; neuroprotective; anti-HIV; human immunodeficiency virus;
KW anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
XX Homo sapiens.
OS

```

```

XX XX WO200152890-A1.
XX XX
XX XX 26-JUL-2001.
PD XX
XX XX 18-JAN-2001; 2001WO-US01825.
XX XX
XX XX 21-JAN-2000; 2000US-0489216.
XX XX
XX XX (UYCO-) UNIV CONNECTICUT HEALTH CENT.
XX XX
XX XX Srivastava PK;
XX XX
XX XX WPI; 2001-451897/48.
XX XX
XX XX Heat shock protein and antigenic molecule complexes, useful for the
PT prevention and treatment of neurodegenerative disorders e.g. senile
PT dementia, Alzheimer's disease and epilepsy -
XX XX
XX XX Disclosure: Page 13; 65pp; English.
XX XX
XX XX The present invention relates to pharmaceutical compositions comprising
CC complexes of heat shock proteins (hsps) in association with antigenic
CC molecules for use in treatment and prevention of neurodegenerative
CC disorders and diseases. The complexes of hsp and antigenic peptides are
CC used as vaccines for the treatment or prevention of neurodegenerative
CC disorders e.g. Alzheimer's disease, age-related loss of cognitive
CC function, senile dementia, Parkinson's disease, amyotrophic lateral
CC sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear
CC palsy, Guam disease, Lewy body dementia, prion diseases, spongiform
CC encephalopathies, Creutzfeldt-Jakob disease, polyglutamine diseases,
CC Huntington's disease, myotonic dystrophy, Friedreich's ataxia, ataxia,
CC Gilles de la Tourette's syndrome, seizure disorders, epilepsy, chronic
CC seizure disorder, stroke, brain trauma, spinal cord trauma, acquired
CC immunodeficiency syndrome (AIDS) dementia, alcoholism, autism, retinal
CC ischaemia, glaucoma, autonomic function disorder, hypertension,
CC neuropsychiatric disorder, schizophrenia or schizoaffective disorder
CC and for eliciting an immune response. The present sequence is human
CC peptide antigen comprising beta amyloid (Abeta) 40.
XX XX
XX XX Sequence 40 AA:
SQ

```

Query Match 100.0%; Score 209; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
    |||||||
DB 1 daefrhdsgyevhghklvfaedvgsnkgaiiglmvgvv 40

```

RESULT 14
AAB84426
ID AAB84426 standard; peptide; 40 AA.
XX
XX AAB84426;
AC
XX
XX 22-AUG-2001 (first entry)
XX
XX Partial sequence of a human beta-amyloid precursor protein.
XX
XX Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
XX vaccine.
XX
XX Homo sapiens.
XX
XX WO200142306-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US33203.
XX

```

PR 08-DEC-1999; 99US-0169687.
XX XX
XX XX (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
XX XX
XX XX Chain B;
XX XX
XX XX WPI; 2001-381648/40.
XX XX
XX XX Novel chimeric peptide containing N- or C-terminal end-specific B cell
PT epitope from naturally occurring internal peptide cleavage product
PT (such as beta amyloid peptide) of a precursor protein, joined to T cell
PT epitope -
XX XX
XX XX Claim 3; Page 41; 47pp; English.
XX XX
XX XX The present sequence represents a partial sequence of a human
CC beta-amyloid precursor protein (APP). The peptide is used to create
CC chimeric peptides of the invention. The chimeric peptides contain a N-
CC or C-terminal end-specific B cell epitope from a naturally occurring
CC internal peptide cleavage product of a precursor or mature protein, as
CC a free N- or C-terminus, joined to a T cell epitope, with or without a
CC spacer amino acid residue. Chimeric peptides comprising betaAP peptides
CC slow down, reduce or prevent the accumulation of amyloid beta peptide in
CC the extracellular space, interstitial fluid and cerebrospinal fluid of
CC the brain, and aggregation into senile amyloid deposits or plaques. They
CC also block the interaction of amyloid beta peptides with other molecules
CC that contribute to the neurotoxicity of amyloid beta. The chimeric peptides
CC are useful for immunizing humans against the free N- or C-terminus of
CC an internal self peptide cleavage product (e.g. APP peptide) derived from
CC a precursor protein or a mature protein. The internal peptide cleavage
XX product is the self molecule of the mammal.
XX
XX Sequence 40 AA:
SQ

```

Query Match 100.0%; Score 209; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
    |||||||
DB 1 daefrhdsgyevhghklvfaedvgsnkgaiiglmvgvv 40

```

RESULT 15
AAB91780
ID AAB91780 standard; Peptide; 40 AA.
XX
XX AAB91780;
AC
XX
XX 22-JUN-2001 (first entry)
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:956.
XX
XX Protection; endogenous therapeutic peptide; peptidease; conjugation;
XX blood component; modification; succinimidyl; maleimide group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
XX
XX 10-SEP-1999; 99US-0153406.
XX
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
XX

PI Bridon DF, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.

XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX
 PS Disclosure; Page 506; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 40 AA;

Query Match 100.0%; Score 209; DB 22; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGGVV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 daefrhdsgyevhqqklyvfaedvgsnkgaliglmvgvv 40

Search completed: April 24, 2002, 09:17:36
 Job time: 140 sec


```
RESULT 2
US-08-235-400-2
Sequence 2, Application US/08235400
Patent No. 5352426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Monn, James A.
APPLICANT: Zimmerman, Dennis M.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-2

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 3
US-08-476-464A-2
Sequence 2, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: RYDEL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREM LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 4
US-08-304-585-1
Sequence 1, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantlyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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US-08-304-585-1

Query Match 100.0%; Score 209; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 5

US-08-302-808-3
; Sequence 3, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhltro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302, 808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286885/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-3

Query Match 100.0%; Score 209; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 6

US-08-433-734-1
; Sequence 1, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110,00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-734-1

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 7

US-08-609-090-8
; Sequence 8, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: ARSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER

Query Match 100.0%; Score 209; DB 1; Length 40;

STREET: 99 Canal Center Plaza, Suite 300
City: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-8

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHQQKLVFAEDVGNKGAIIIGLMVGCV 40
Db 1 DAERHDSGYEVHQQKLVFAEDVGNKGAIIIGLMVGCV 40

RESULT 8
US-07-737-371E-69
Sequence 69, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-69

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHQQKLVFAEDVGNKGAIIIGLMVGCV 40
Db 1 DAERHDSGYEVHQQKLVFAEDVGNKGAIIIGLMVGCV 40

RESULT 9
US-08-682-245A-2
Sequence 2, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U S A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-2

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
|||||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 10
US-08-986-948-3
; Sequence 3, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uh1ro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-3

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
|||||

RESULT 11
US-08-461-216-1
; Sequence 1, Application US/08461216
; Patent No. 5958883
; GENERAL INFORMATION:
; APPLICANT: SNOW, A.D.
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOFW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: [SYMBOL 98 \f "Symbol"]/A4(1-40);
; DESCRIPTION: FIGURES 23-29
; US-08-461-216-1

Query Match 100.0%; Score 209; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
|||||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 12
US-08-959-148-1
; Sequence 1, Application US/08959148
; Patent No. 6172277
; GENERAL INFORMATION:
; APPLICANT: Tate, Barbara A.
; APPLICANT: Majocha, Ronald
; APPLICANT: Newton, Julie L.
; TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
; FILE REFERENCE: 04930/022001
; CURRENT APPLICATION NUMBER: US/08/959,148

;; CURRENT FILING DATE: 1997-10-28
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 40
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-959-148-1

Query Match 100.0%; Score 209; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 13
PCT-US92-06700-1
Sequence 1, Application PC/TUS9206700
GENERAL INFORMATION:
APPLICANT: Mantyh, Patrick W.
APPLICANT: Magglio, John E.
TITLE OF INVENTION: Labeled -Amyloid Peptide
TITLE OF INVENTION: and Alzheimer's Disease Detection
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Northwest Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
COMPUTER: Northgate 386
OPERATING SYSTEM: DOS 4.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06700
FILING DATE: 19920810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.226-WO-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Internal fragment of the
NAME/KEY: amyloid peptide precursor
LOCATION: Represents isolated internal
LOCATION: sequence of 40 amino acid residues from
LOCATION: the amyloid peptide precursor
PCT-US92-06700-1

Query Match 100.0%; Score 209; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 14
US-08-302-808-4
Sequence 4, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 SPRE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-4

Query Match 100.0%; Score 209; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 15

US-08-682-245A-3

; Sequence 3, Application US/08682245A

; Patent No. 5919631

; GENERAL INFORMATION:

; APPLICANT: GOYAL, SHEFALI

; APPLICANT: PAUL, JOSEPH W

; APPLICANT: RIEDEL, NORBERT G

; APPLICANT: SAHASRABUDHE, SUDHIR

; TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOECHST MARION ROUSSEL, INC.

; STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300

; CITY: CINCINNATI

; STATE: OHIO

; COUNTRY: U.S.A.

; ZIP: 45215-6300

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/682,245A

; FILING DATE: 17-JUL-1996

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 60/039,414

; FILING DATE: 16-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: LENTZ, NELSEN L

; REGISTRATION NUMBER: 38,537

; REFERENCE/DOCKET NUMBER: HR-1257A

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; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 41 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-682-245A-3

Query Match 100.0%; Score 209; DB 2; Length 41;

Best Local Similarity 100.0%; Pred No. 2,4e-25;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGCV 40
|||||
Db 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGCV 40

Search completed: April 24, 2002, 09:18:15
Job time: 174 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:15:41 ; Search time 38.71 Seconds
(without alignments)
78.713 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	42	2	beta-amyloid prote
2	209	100.0	57	2	Alzheimer's diseas
3	209	100.0	57	2	Alzheimer's diseas
4	209	100.0	57	2	Alzheimer's diseas
5	209	100.0	57	2	Alzheimer's diseas
6	209	100.0	57	2	Alzheimer's diseas
7	209	100.0	57	2	Alzheimer's diseas
8	209	100.0	82	2	Alzheimer's diseas
9	209	100.0	695	1	Alzheimer's diseas
10	209	100.0	770	1	Alzheimer's diseas
11	190	90.9	695	2	Alzheimer's diseas
12	190	90.9	695	2	Alzheimer's diseas
13	190	90.9	747	2	Alzheimer's diseas
14	133	63.6	33	2	Alzheimer's diseas
15	57	27.3	327	2	beta-amyloid prote
16	56.5	27.0	378	2	genome polyprotein
17	55.5	26.6	678	2	Slc1 protein - yea
18	55	26.3	488	2	3-methyl-2-oxobuta
19	55	26.3	503	2	probable aldehyde
20	55	26.3	755	1	general amino acid
21	55	26.3	3063	2	tryptophan 2-mono
22	54.5	26.1	678	2	genome polyprotein
23	54.5	26.1	832	2	3-methyl-2-oxobuta
24	54	25.8	284	2	phospholipase D 1
25	54	25.8	755	1	genome polyprotein
26	53.5	25.6	708	1	tryptophan 2-mono
27	53.5	25.6	971	2	hypothetical prote
28	53	25.4	256	2	conserved hypotnet
29	53	25.4	422	2	hypothetical prote

30	53	25.4	601	2	T02581	nodulin-like prote
31	53	25.4	1555	2	JT0959	polyprotein - pota
32	52.5	25.1	678	2	C86495	hypothetical prote
33	52.5	25.1	678	2	H72128	3-methyl-2-oxobuta
34	52	24.9	272	2	F70979	hypothetical prote
35	52	24.9	417	2	F70132	conserved hypotnet
36	52	24.9	527	2	T18232	formylmethanofuran
37	51.5	24.6	297	2	G69525	cation transporter
38	51.5	24.6	314	2	F86805	probable xanthine
39	51.5	24.6	1364	2	T51920	sugr protein - Del
40	51	24.4	103	2	D75449	probable cobq prot
41	51	24.4	494	2	C70940	nuclear inclusion
42	50.5	24.2	519	2	PC1072	probable phospholi
43	50.5	24.2	833	2	T01547	tegument protein 7
44	50.5	24.2	1345	2	S55669	naphthocate synthas
45	50	23.9	285	1	B64105	

ALIGNMENTS

RESULT 1

PN0512 beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 209; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-21;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40
DB 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40

RESULT 2

E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40
DB 6 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 45

RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; M0ID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; M0ID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; M0ID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; M0ID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; M0ID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; M0ID:93075180

A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAB>
 A:Cross-references: GB:M83556; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 209; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 4.8e-21;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGEVHHQKLVFAEDVGSNKGATIGLVGCV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 17 DAEFRHDSGEVHHQKLVFAEDVGSNKGATIGLVGCV 56

RESULT 9
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AA36629.1; PID:9342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 209; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 5e-20;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGEVHHQKLVFAEDVGSNKGATIGLVGCV 40
 ||||||||||||||||||||||||||||||||||||||||
 Db 597 DAEFRHDSGEVHHQKLVFAEDVGSNKGATIGLVGCV 636

RESULT 10
 Q8HND4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
 4668; A28583; A29302; A60805; J00388; S06121; A60355; A59011; A38384; S29076; S38522; S3
 R:Lehman, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Beyne, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PEDA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lehman, H.G.

submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360
 A:Note: alternative splice form APP(695)
 R:La Paoli, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA313654.1; PID:9516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AA51768.1; PID:9178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AA559502.1; PID:9178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPTVPAFPAKVR' <YOS2>
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AA559501.1; PID:9178615
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AA51727.1; PID:9178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AA119991.1; PID:9236721
 R:Kamano, K.; Orr, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 Arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:q257378
 A:Experimental source: Familial Alzheimer disease family SB
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:q257380
 A:Experimental source: Familial Alzheimer disease family LIT
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115376)
 A:Note: This sequence has a silent mutation
 A:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:q28525; PIDN:CAA68374.1; PID:q28526
 A:Note: Alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540
 A:Note: The authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid A
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:q178707
 A:Experimental source: brain
 R:Ranz, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15352; NID:q177957; PIDN:AAA51564.1; PID:q177958
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 A:Residues: 672-678 <DYR>
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: Alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Demhilly, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
 A:Reference number: S00925; MUID:88122659
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>

A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
 A:Note: Alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q2929611
 A:Experimental source: glioblastoma cell line
 A:Note: Alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
 A:Reference number: A30320
 A:Accession: A30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573
 A:Note: The authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asp, AAT for residue 610 as Gly, and GGT for residue
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 209; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.6e-20;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRDSCGYEVHOKLVFAEDVGSNKGAIITGLMGV 40
 Db 672 DAEFRDSCGYEVHOKLVFAEDVGSNKGAIITGLMGV 711
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence,revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Ramada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
 A:Experimental source: brain
 R:de Strooper, B.; Van Leuven, F.; Van den Berghe, H.
 Biochem. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379
R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MIMD:92209998
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329
C:Genetics:
A:Map position: 16c3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 90.9%; Score 190; DB 2; Length 695;
Best Local Similarity 92.5%; Pred. No. 1.8e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVSNKGAIIIGLMGVV 40
Db 597 DAEFGHDSGEVRRHOKLVFAEDVSNKGAIIIGLMGVV 636

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
M:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MIMD:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CA30488.1; PID:q55617
R:Schubert, D.; Schneider, R.; Jacordiere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MIMD:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MIMD:94320627
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Muller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MIMD:91217087
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 90.9%; Score 190; DB 2; Length 695;
Best Local Similarity 92.5%; Pred. No. 1.8e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVSNKGAIIIGLMGVV 40
Db 597 DAEFGHDSGEVRRHOKLVFAEDVSNKGAIIIGLMGVV 636

RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
A:Reference number: JH0773; MIMD:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:q263150; PIDN:AAB24853.1; PID:q263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 90.9%; Score 190; DB 2; Length 747;
Best Local Similarity 87.5%; Pred. No. 1.9e-17;
Matches 35; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVSNKGAIIIGLMGVV 40
Db 649 DSEVRHDTAVEVHOKLVFAEDVSNKGAIIIGLMGVV 688

RESULT 14
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
A:Reference number: S23094; MIMD:92316198
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KOJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

Query Match 63.6%; Score 133; DB 2; Length 33;
Best Local Similarity 89.3%; Pred. No. 2.7e-11;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVSNK 28
Db 6 DAEFGHDSGEVRRHOKLVFAEDVSNK 33

RESULT 15
S11435
genome polypeptide - potato virus Y (fragment)
N:Contains: coat protein; NIB protein
C:Species: potato virus Y, PVY
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Nov-2000
C:Accession: S11435; S11549; J01526
R:Zhou, X.R.; Fang, R.X.; Wang, C.O.; Wang, K.Q.
Nucleic Acids Res. 18, 5554, 1990
A:Title: CDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).
A:Reference number: S11435; MIMD:91016851
A:Accession: S11435
A:Molecule type: mRNA
A:Residues: 1-327 <ZHO1>

A:Cross-references: EMBL:X54058
 R:Zhou, X.R.
 Submitted to the EMBL Data Library, July 1990
 A:Reference number: S11549
 A:Accession: S11549
 A:Molecule type: mRNA
 A:Residues: 1-90, 'E', 92-327 <2H02>
 A:Cross-references: EMBL:X54058; NID:g61219; PIDN:CAA37993.1; PID:g833159
 R:Ohshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.
 Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991
 A:Title: Comparison of biological properties, serological characteristics and amino acid
 A:Reference number: JC1526
 A:Accession: JC1526
 A:Molecule type: genomic RNA
 A:Residues: 61-68, 'E', 71-73, 'E', 76-111, 'S', 113-201, 'E', 203-327 <OHS>
 C:Genetics:
 A:Start codon: GCA
 C:Superfamily: tobacco etch virus genome polyprotein
 C:Keywords: coat protein; polyprotein
 F:61-327/Product: coat protein #status predicted <COP>

Query Match 27.38; Score 57; DB 2; Length 327;
 Best Local Similarity 53.18; Pred. No. 5;
 Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;
 QY 1 DAEFRHDSGYEVHHQKLVFFAED---VGSNK 28
 ||| ||||| | | | | |
 Db 47 DDEFEFDS-YEVHHQ-----ANDTIDAVGDNK 72

Search completed: April 24, 2002, 09:19:00
 Job time: 199 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:16:11 ; Search time 62.94 Seconds
(without alignments)
92.960 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAERDSDGYEHHQKLVFAEDVGSNKGAIIGLMGVGV 40

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	209	100.0	82	4	P78438
2	209	100.0	82	4	Q16014
3	209	100.0	82	4	Q16019
4	209	100.0	82	4	Q16020
5	209	100.0	534	13	Q93296
6	209	100.0	569	13	Q9PVL1
7	209	100.0	695	13	Q60496
8	209	100.0	695	13	Q9DGJ7
9	209	100.0	751	13	Q9DGJ7
10	209	100.0	770	6	Q9TUI0
11	199	95.2	97	4	Q13778
12	190	90.9	79	11	Q35463
13	190	90.9	607	11	Q99X32
14	190	90.9	693	13	Q98SG0
15	190	90.9	695	11	P97487
16	190	90.9	747	13	Q91963
17	187	89.5	695	13	Q98SF9
18	180	86.1	699	13	O57394
19	176	84.2	33	4	Q9UC33

073683 tetraodon f
093279 fugu rubrip
Q9UCA9 homo sapien
Q919E7 brachydanio
Q9UCD1 homo sapien
Q97917 bos taurus
Q9UCC8 homo sapien
Q9RPS4 enterococcu
Q9AWB6 lycopersico
Q22662 arabidopsis
Q9GQN5 potato viru
Q9WQ05 potato viru
O81120 lotus japon
Q9R717 agrobacteri
Q9R694 agrobacteri
Q9R472 agrobacteri
O84344 chlamydia t
Q44388 agrobacteri
Q9PK54 chlamydia m
Q9XGT0 gossypium h
P93745 arabidopsis
P93733 arabidopsis
Q85276 potato viru
Q9CA59 arabidopsis
O50548 thermotoga
O80960 arabidopsis

ALIGNMENTS

RESULT 1

P78438

ID P78438 PRELIMINARY; PRT; 82 AA.

AC P78438;

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).

GN APP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89392030; PubMed=2675837;

RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H., Little S.P.;

RA "Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.";

RT Biochem. Biophys. Res. Commun. 163:1248-1255(1989).

RL [2]

RN [2]

RP SEQUENCE OF 19-48 FROM N.A.

RX MEDLINE=87120329; PubMed=2949367;

RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P., Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;

RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.";

RL Science 235:880-884(1987).

RN [3]

RP SEQUENCE OF 32-63 FROM N.A.

RX MEDLINE=93035397; PubMed=1415269;

RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M., Anderson L., O'dahl S., Nemens E., White J.A.;

RT "Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.";

RL Am. J. Hum. Genet. 51:998-1014(1992).

DR EMBL; M29270; AAA51768.1; -

DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL; M15532; AAA51564.1; -

DR EMBL; S45136; AAB23646.1; -

DR HSP; P05067; 1BA4.

FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 40
DB 17 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 56

RESULT 2
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -
DR HSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 40
DB 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 57

RESULT 3
Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).
OS BETA APP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 40
DB 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 57

RESULT 4
Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -
DR HSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 40
DB 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLWGVV 57

RESULT 5
Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLLOID PRECURSOR PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a substrate for Caspase 3 in dying motoneurons.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042098; AAC35052.1; -
DR HSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match 100.0%; Score 209; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40
|||||
Db 436 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 475

RESULT 6

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 209; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40
|||||
Db 472 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 511

RESULT 7

ID Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Beck M., Mueller D., Bigl V.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC GIO).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.

DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 209; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40
|||||
Db 597 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 636

RESULT 8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 209; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40
|||||
Db 597 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 636

RESULT 9

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.

```

OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
   isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RC -!- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AF289219; AAG00594.1; -.
DR InterPro: IPR001868; A4_APP.
DR pfam: PF02177; A4_EXTRA; 1.
DR pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; BASICPTASE.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match          100.0%; Score 209; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 692

RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RC -!- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AB032550; BAA84580.1; -.
DR HSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR pfam: PF02177; A4_EXTRA; 1.
DR pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match          100.0%; Score 209; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

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DB 672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 711

RESULT 11
Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
   brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL: M15533; AAA35540.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA4.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match          95.2%; Score 199; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EPRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 EPRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 38

RESULT 12
Q35463 PRELIMINARY; PRT; 79 AA.
AC Q35463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSP: P05067; IQCM.
DR NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF597 CRC64;

Query Match          90.9%; Score 190; DB 11; Length 79;
Best Local Similarity 92.5%; Pred. No. 6.5e-18;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 21 DAEFGHDSGFVRHOKLVFFAEDVGSNKGAIIGLMVGVV 60

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RESULT 13
Q99K32 ID Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,
RA Loring J.F., Goate A.M.,
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -
DR EMBL; U82624; AAB40919.1; -
DR HSSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 90.9%; Score 190; DB 11; Length 607;
Best Local Similarity 92.5%; Pred. No. 7.5e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 DAEFGHDSGFVRRHQKLVFFAEDVGSNKGAIIGLMVGGVV 548

RESULT 14
Q98SG0 ID Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -
KW Signal.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 90.9%; Score 190; DB 13; Length 693;
Best Local Similarity 87.5%; Pred. No. 8.8e-17;
Matches 35; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
1:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 595 DSEYRHTAYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 634

RESULT 15
P97487 ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

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DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,
RA Loring J.F., Goate A.M.,
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -
DR EMBL; U82624; AAB40919.1; -
DR HSSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 90.9%; Score 190; DB 11; Length 695;
Best Local Similarity 92.5%; Pred. No. 8.9e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 597 DAEFGHDSGFVRRHQKLVFFAEDVGSNKGAIIGLMVGGVV 636

Search completed: April 24, 2002, 09:20:10
Job time: 239 sec

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:16:26 ; Search time 21.42 Seconds
(without alignments)
68.468 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	209	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	209	100.0	57	1 A4_URDMA	Q29149 ursus marit
3	209	100.0	58	1 A4_CANFA	Q28280 canis faml
4	209	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	209	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	209	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	209	100.0	751	1 A4_SALSC	Q95241 salmisi sci
8	209	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	190	90.9	770	1 A4_MOUSE	P12023 mus musculu
10	190	90.9	770	1 A4_RAT	P08592 rattus norv
11	57	27.3	327	1 POLG_PVYCH	P21294 potat viru
12	56.5	27.0	378	1 SLGL_YEAST	P54867 saccharomyc
13	55	26.3	488	1 DHAL_PESP	P33008 pseudomonas
14	55	26.3	503	1 Y226_MYCPN	P73462 mycoplasma
15	55	26.3	755	1 TR2M_AGR74	Q04029 agrobacteri
16	55	26.3	3063	1 POLG_PVYN	P18247 p genome po
17	54	25.8	284	1 POLG_PVYTO	P11897 potat viru
18	54	25.8	755	1 TR2M_AGR73	P25017 agrobacteri
19	53.5	25.6	708	1 YNZB_CAEEL	P45972 caenorhabdi
20	53.5	25.6	971	1 Y228_BORBU	O51246 borrelia bu
21	51.5	24.6	297	1 FTR_ARCFU	O28076 archaeoglob
22	51	24.4	494	1 COBQ_MYCTU	O53677 mycobacteri
23	50	23.9	285	1 MENB_HAEIN	P44960 haemophilus
24	49	23.4	568	1 NIRS_PSEAE	P24592 pseudomonas
25	49	23.4	611	1 YCR3_YEAST	P25351 saccharomyc
26	49	23.4	704	1 SSP2_BOMMO	P20613 bombyx mori
27	49	23.4	753	1 PEE2_HUMAN	O14830 homo sapien
28	49	23.4	757	1 PEE2_MOUSE	O35385 mus musculu
29	49	23.4	769	1 ITB2_BOVIN	P32592 bos taurus
30	49	23.4	1080	1 HOC_DROME	Q9n2m8 drosophila
31	49	23.4	1437	1 MRP5_HUMAN	O15440 homo sapien
32	48.5	23.2	160	1 FMDR_ECOLI	P24093 escherichia
33	48.5	23.2	330	1 COAT_PEMV	P07993 pepper mott

34	48.5	23.2	393	1 GUN1_USTMA	P54424 ustilago ma
35	48.5	23.2	510	1 YM43_YEAST	Q03218 saccharomyc
36	48	23.0	409	1 RHAG_HUMAN	Q02094 homo sapien
37	48	23.0	703	1 ARVB_WANSE	P14297 manduca sex
38	48	23.0	930	1 DPOL_HAEIN	P43741 haemophilus
39	47.5	22.7	251	1 FGEN_HUMAN	Q9gzv9 homo sapien
40	47.5	22.7	1052	1 RPOC_BACAN	P77819 bacillus an
41	47.5	22.7	1053	1 RPOC_BROTH	P77839 brochothrix
42	47	22.5	119	1 YVAE_BACSU	Q32227 bacillus su
43	47	22.5	247	1 EST_BACST	O36174 bacillus st
44	47	22.5	478	1 G6PD_BORBU	O51581 borrelia bu
45	47	22.5	560	1 NIRS_PSEST	P24040 pseudomonas

ALIGNMENTS

RESULT	1	
ID	A4_PIG	STANDARD; PRT; 57 AA.
AC	Q29023;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	20-AUG-2001 (Rel. 40, Last annotation update)	
DE	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID	
DE	PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).	
GN	APP.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Brain;	
RX	MEDLINE=92017079; PubMed=1656157;	
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;	
RT	"Conservation of the sequence of the Alzheimer's disease amyloid	
RT	peptide in dog, polar bear and five other mammals by cross-species	
RT	polymerase chain reaction analysis.";	
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).	
CC	!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO	
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN	
CC	G(O) (BY SIMILARITY).	
CC	!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	!- SIMILARITY: BELONGS TO THE APP FAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	or send an email to license@isb-sib.ch).	
CC	-----	
CC	EMBL; X56127; CAA39592.1; -	
DR	HSSP; P05067; 1AML.	
DR	InterPro; IPR001868; A4_APP.	
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.	
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.	
DR	Glycoprotein; Amyloid; Neuron; Transmembrane.	
FT	NON_TER 1 1	
FT	CHAIN 6 48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN <1 33	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 34 57	POTENTIAL.
FT	NON_TER 57 57	
SQ	SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;	

Query Match 100.0%; Score 209; DB 1; Length 57;
Best Local Similarity 100.0%; Pred No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 45
|||||

RESULT 2

A4_URSMA ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57
FT NON_TER 57 57
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 209; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 40
|||||

RESULT 3

A4_CANFA ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X56128; CAA39593.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57
FT NON_TER 57 57
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 209; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 40
|||||

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 45
|||||

GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56125; CAA39590.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 209; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 40
|||||

Db 7 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 46
|||||

RESULT 4

A4_RABIT ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56125; CAA39590.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 209; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 40
|||||

Db 7 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGWV 46
|||||

RESULT 4

A4_RABIT ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56125; CAA39590.1; -
CC HSSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;


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FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSMEM 35 58
FT DOMAIN 59 >59
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 209; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHVKLVFFAEDVGSNGKGAIGLVMGVV 40
    |||||
DB 7 DAEFRHDSGYEVHVKLVFFAEDVGSNGKGAIGLVMGVV 46

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP.
OS Samirli sclereus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC !- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC !- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC !- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC !- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC
CC -----
CC EMBL; S81024; AAD14347.1; .
CC InterPro; IPR001868; A4_APP.
CC DR InterPro; IPR002223; Kunitz_BPTI.
CC DR Pfam; PF02177; A4_EXTRA; 1.
CC DR Pfam; PF00014; Kunitz_BPTI; 1.
CC DR PRINTS; PR00203; AMYLOIDA4.
CC DR PRINTS; PR00204; BETAAMYLOID.
CC DR PRINTS; PR00759; BASICPTASE.
CC DR SMART; SM00006; A4_EXTRA; 1.
CC DR SMART; SM00131; KU; 1.
CC DR PROSITE; PS00319; A4_EXTRA; 1.
CC DR PROSITE; PS00320; A4_INTRA; 1.
CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 209; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHVKLVFFAEDVGSNGKGAIGLVMGVV 40
    |||||
DB 653 DAEFRHDSGYEVHVKLVFFAEDVGSNGKGAIGLVMGVV 692

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
DE (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,

```

RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RL sequencing of a 300 kb region of human APP locus.";
 RN Nucleic Acids Res. 25:1802-1808(1997).
 [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=8812640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=8812641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX TISSUE=Liver;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).
 [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=9318965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;

RA Dyrks T., Weidemann A., Muthaupt G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
RL EMBO J. 7:949-957(1988).
RN [24]
RP REVIEW.
RX MEDLINE=92271194; PubMed=1589757;
RA Kosik K.S.;
RT "Alzheimer's disease: a cell biological perspective.";
RL Science 256:780-783(1992).
RN [25]

Query Match 100.0%; Score 209; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGGV 40
DB 672 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGGV 711

RESULT 9

A4_MOUSE
ID A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
DC 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN=BALE/C; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH XIL-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL; X59379; -; NOT ANNOTATED_CDS.
DR EMBL; M18373; AAA37139.1; -;
DR EMBL; X15210; CRA33280.1; -;
DR EMBL; D10603; BAA01456.1; -;
DR EMBL; M24397; AAA39929.1; -;
DR PIR; A27485; A27485.
DR PIR; S04855; S04855.
DR PIR; S19727; S19727.
DR MGI; 88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 770 770
FT CYTOPLASMIC (POTENTIAL).
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 673 715
FT DOMAIN 287 345
FT BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
FT CLATHRIN-BINDING (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT E -> V (IN ISOFORM APP(695)).
FT MISSING (IN ISOFORM APP(695)).
FT VARSPLIC 290 364
FT VARSPLIC 346 380
FT MISSING (IN ISOFORM APP(751)).
FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;
SQ


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Query Match          90.9%; Score 190; DB 1; Length 770;
Best Local Similarity 92.5%; Pred. No. 1.le-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGVEVHHQKLVFFAEDVGSNGKAIIGLMVGWV 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 672 DAEFGHDSGFEVHRQKLVFFAEDVGSNGKAIIGLMVGWV 711

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-DEC-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE (ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
  (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RL Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
  in rat brain suggests a role in cell contact.";
RT EMBO J. 7:1365-1370(1988).
[2]
SEQUENCE OF 289-364 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
  APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
  SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
  PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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  or send an email to license@isb-sib.ch).
-----
CC EMBL; X07648; CAA30488.1; -.
CC EMBL; X14066; CAA32229.1; -.
CC PIR; S00550; S00550.
CC PIR; S03607; S03607.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00204; BETAAMYLOID.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00006; A4_EXTRA; 1.

Query Match          90.9%; Score 190; DB 1; Length 770;
Best Local Similarity 92.5%; Pred. No. 1.le-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGVEVHHQKLVFFAEDVGSNGKAIIGLMVGWV 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 672 DAEFGHDSGFEVHRQKLVFFAEDVGSNGKAIIGLMVGWV 711

RESULT 11
POLG_PVYCH
ID POLG_PVYCH STANDARD; PRT; 327 AA.
AC P21294;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)
  (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]
  (FRAGMENT).
DE Potato virus Y (strain Chinese isolate) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12218;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=91016851; PubMed=2216735;
RA Zhou X.R., Fang R.X., Wang C.Q., Mang K.Q.;
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese
  isolate).";
RL Nucleic Acids Res. 18:5554-5554(1990).
CC -!- PWM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
  POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
  PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
  INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
-----
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  or send an email to license@isb-sib.ch).
-----
CC EMBL; X54058; CAA37993.1; -.
CC PIR; S11549; S11549.
CC HSSP; P05067; IAMB.
```

DR InterPro; IPR001592; Poty_coat.
 KW Pfam; PF00767; Poty_Coat; 1.
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
 FT NON_TER 1 60 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 61 327 COAT PROTEIN.
 FT CHAIN 61 327 COAT PROTEIN.
 SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DE62F18 CRC64;

Query Match 27.3%; Score 57; DB 1; Length 327;
 Best Local Similarity 53.1%; Pred. No. 2.5;

Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDV---VGSNK 28
 DB 47 DDEFEEDS-YEVHHQ-----NDTIDAVGDNK 72

RESULT 12

ID SLG1_YEAST STANDARD; PRT; 378 AA.
 AC P54867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SLG1 PROTEIN PRECURSOR.
 GN SLG1 OR YOR008C OR UNF378.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA de Bettignies G., Bergez-Aullo P., Barthe C., Louvet O.,
 RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
 RA Peypouquet M.F., Morel C., Dolignon F., Crouzet M.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97051599; PubMed=8896276;
 RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
 RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
 from Saccharomyces cerevisiae reveals 15 open reading frames, five of
 which correspond to previously identified genes.";
 RL Yeast 12:1091-1095(1996).

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DR EMBL; U39481; AAA85862.1; -
 DR EMBL; U43491; AAC49488.1; -
 DR EMBL; 274916; CAA99196.1; -
 DR HSSP; P05067; 1BA6.
 DR SGD; S0005534; SLG1.
 DR InterPro; IPR002889; WSC.
 DR Pfam; PF01822; WSC; 1.
 DR SMART; SM00321; WSC; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 378 SLG1 PROTEIN.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 378 AA; 39270 MW; EE164F2374CCCE3 CRC64;

Query Match 27.0%; Score 56.5; DB 1; Length 378;
 Best Local Similarity 42.4%; Pred. No. 3.4;

Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

OY 8 SGYEVHHQKLVFFAEDVGSNKGAIGLMVGWV 40
 DB 251 SGSKTHKKK-----ANVAIGVGVGVW 274

RESULT 13

ID DHAL_PSESP STANDARD; PRT; 488 AA.
 AC P33008;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PROBABLE ALDEHYDE DEHYDROGENASE (EC 1.2.1.3).
 GN TERPE.
 OS Pseudomonas sp.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92332528; PubMed=1629218;
 RA Peterson J.A., Lu J.-Y., Geisselsoder J., Graham-Lorence S.,
 RA Carmona C., Witney F., Lorence M.C.;
 RT "Chromatome P-450terp. Isolation and purification of the protein and
 RT cloning and sequencing of its operon.";
 RL J. Biol. Chem. 267:14193-14203(1992).
 CC -!- FUNCTION: INVOLVED IN A ALPHA-TERPENEOL OXIDATION SYSTEM.
 CC -!- CATALYTIC ACTIVITY: ALDEHYDE + NAD(+) + H(2)O = ACID + NADH.
 CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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DR EMBL; M91440; AAA25995.1; -
 DR PIR; S27652; S27652.
 DR PIR; C42971; C42971.
 DR HSSP; P20000; 1A4Z.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldehyd; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Oxidoreductase; NAD.
 FT NP_BIND 240 245 NAD (ADP PART) (BY SIMILARITY).
 FT ACT_SITE 262 262 BY SIMILARITY.
 FT ACT_SITE 296 296 BY SIMILARITY.
 SQ SEQUENCE 488 AA; 52156 MW; 2144AE1B173C854 CRC64;

Query Match 26.3%; Score 55; DB 1; Length 488;
 Best Local Similarity 40.6%; Pred. No. 7;

Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

OY 6 HDSGYEVHHQKLVFFAEDV---GSNKGAIG 33
 DB 305 HESIYAFRDLKLVAYAQNVVIGDGSGPGVTMG 336

RESULT 14

ID Y226_MYCPN STANDARD; PRT; 503 AA.
 AC P75462;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN MG226 HOMOLOG (F10_ORF503).
 GN MPN319 OR MP517.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.

```

NCBI_TaxID=2104;
[1]
RN  SEQUENCE FROM N.A.
RP  PLASMID=PTIA6NC;
RX  MEDLINE=84170374; PubMed=6584906;
RA  Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
RA  Fuller S., Flores C., Peschon J., Nestor E., Gordon M.;
RA  Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA  Herrmann R.;
RT  "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT  pneumoniae.";
RL  Nucleic Acids Res. 24:4420-4449(1996).
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC  -!- SIMILARITY: TO M.GENITALIUM MG225.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AE000051; AAB96165.1; -
DR  InterPro: IPR002293; AA_rel_permease_1.
DR  InterPro: IPR002027; Amino_acid_permease.
DR  Pfam: PF00324; aa_permeases; 1.
KW  Hypothetical protein; Transmembrane; Complete proteome.
FT  TRANSMEM 20 40 POTENTIAL.
FT  TRANSMEM 43 63 POTENTIAL.
FT  TRANSMEM 106 126 POTENTIAL.
FT  TRANSMEM 138 158 POTENTIAL.
FT  TRANSMEM 166 186 POTENTIAL.
FT  TRANSMEM 215 235 POTENTIAL.
FT  TRANSMEM 249 269 POTENTIAL.
FT  TRANSMEM 301 321 POTENTIAL.
FT  TRANSMEM 359 379 POTENTIAL.
FT  TRANSMEM 405 425 POTENTIAL.
FT  TRANSMEM 443 463 POTENTIAL.
FT  TRANSMEM 468 488 POTENTIAL.
SQ  SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match      26.3%; Score 55; DB 1; Length 503;
Best Local Similarity 64.7%; Pred. No. 7.2;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  24 VGSNKGAIIGLMVGVV 40
DB  131 VKDNGALIGLLVGGFV 147

RESULT 15
TR2M_AGR74
ID  TR2M_AGR74 STANDARD; PRT; 755 AA.
AC  P04029;
DT  23-OCT-1986 (Rel. 02, Created)
DT  23-OCT-1986 (Rel. 02, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  TRYPTOPHAN 2-MONOOXYGENASE (EC 1.13.12.3).
GN  TMS1.
OS  Agrobacterium tumefaciens.
OG  Plasmid pTiAch5, and Plasmid pTiA6NC.
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Rhizobiaceae; Rhizobium.
OX  NCBI_TaxID=358;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=84207942; PubMed=6327292;
RA  Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
RA  Lemmers M., van Montagu M., Schell J.;
RT  "The complete nucleotide sequence of the TL-DNA of the Agrobacterium
RT  tumefaciens plasmid pTiAch5.";
RL  EMBO J. 3:835-846(1984).
```

```

[2]
RN  SEQUENCE FROM N.A.
RP  PLASMID=PTIA6NC;
RX  MEDLINE=84170374; PubMed=6584906;
RA  Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
RA  Fuller S., Flores C., Peschon J., Nestor E., Gordon M.;
RA  Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA  Herrmann R.;
RT  "Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti
RT  plasmid: two gene products involved in plant tumorigenesis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
CC  -!- CATALYTIC ACTIVITY: L-TRYPTOPHAN + O(2) -> INDOLE-3-ACETAMIDE +
CC  CO(2) + H(2)O.
CC  -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
CC  -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.
CC  -!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC  P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC  THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC  -!- SIMILARITY: STRONG, WITH ITS A.TUMEFACIENS PLASMID PTITM4
CC  COUNTERPART.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: K02554; AAA92550.1; -
DR  PIR: A04497; QOAG4T.
DR  InterPro: IPR002937; Amino_Oxidase.
DR  InterPro: IPR00205; NAD_binding.
DR  Pfam: PF01593; Amino_Oxidase; 1.
KW  Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
KW  T-DNA; Plasmid.
FT  VARIANT 718 719 NR -> IQ (IN PTIA6NC).
FT  VARIANT 721 721 P -> A (IN PTIA6NC).
SQ  SEQUENCE 755 AA; 83947 MW; 9FD2B83FEA001A4D CRC64;

Query Match      26.3%; Score 55; DB 1; Length 755;
Best Local Similarity 41.2%; Pred. No. 11;
Matches 14; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

QY  7 DSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVV 40
DB  223 DSG-----RIGFFEDVPKPKVAVIGAGISGLV 250
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Search completed: April 24, 2002, 09:20:38
Job time: 252 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:50 ; Search time 66.52 Seconds
(without alignments)
12.249 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 11
Sequence: 1 GSNKGAIIGLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
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18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	11	100.0	11	15	AA60369		Beta-amyloid (25-3
2	11	100.0	11	16	AA87948		beta-amyloid (25-3
3	11	100.0	11	17	AA92807		Human beta-amyloid
4	11	100.0	11	18	AAW2336		Amyloid beta pepti
5	11	100.0	11	19	AAW64497		Neurotoxic beta-am
6	11	100.0	11	19	AAW47231		Beta-amyloid pepti
7	11	100.0	11	20	AAW81470		Synthetic amyloid
8	11	100.0	11	21	AAV52133		Human Receptor to
9	11	100.0	11	22	AA81775		Amyloid beta-prote
10	11	100.0	11	22	AA81808		Amyloid beta-prote
11	11	100.0	14	19	AAW64498		Neurotoxic beta-am

12	11	100.0	14	22	AA891782		Amyloid beta-prote
13	11	100.0	14	22	AA891788		Amyloid beta-prote
14	11	100.0	14	22	AA891815		Amyloid beta-prote
15	11	100.0	24	22	AA891805		Amyloid beta-prote
16	11	100.0	24	22	AA891832		Amyloid beta-prote
17	11	100.0	26	19	AAW47229		Beta-amyloid pepti
18	11	100.0	26	20	AAV33408		Human amyloidogeni
19	11	100.0	26	22	AA84431		Partial sequence o
20	11	100.0	27	20	AAV33409		Human amyloidogeni
21	11	100.0	32	22	AA84430		Partial sequence o
22	11	100.0	35	17	AAW02336		Beta-amyloid pepti
23	11	100.0	35	19	AAW47228		Beta-amyloid pepti
24	11	100.0	35	20	AAW89356		Beta-amyloid pepti
25	11	100.0	35	20	AAW89357		Beta-amyloid pepti
26	11	100.0	35	20	AAW89360		Beta-amyloid pepti
27	11	100.0	35	20	AAW89361		Beta-amyloid pepti
28	11	100.0	35	22	AA891803		Amyloid beta-prote
29	11	100.0	35	22	AA891830		Amyloid beta-prote
30	11	100.0	36	20	AAW81471		Synthetic amyloid
31	11	100.0	38	15	AA60362		Beta-amyloid (1-38
32	11	100.0	38	20	AAW92722		Human tachykinin a
33	11	100.0	38	22	AA891799		Amyloid beta-prote
34	11	100.0	38	22	AA891826		Amyloid beta-prote
35	11	100.0	39	15	AA60363		Beta-amyloid (1-39
36	11	100.0	39	20	AAV25134		Human amyloid beta
37	11	100.0	39	20	AAW81472		Synthetic amyloid
38	11	100.0	39	21	AAV52132		Human Receptor to
39	11	100.0	40	14	AA833191		Beta-amyloid pepti
40	11	100.0	40	15	AA60364		Beta-amyloid (1-40
41	11	100.0	40	18	AAW37507		Amyloid beta prote
42	11	100.0	40	18	AAW23335		Amyloid beta pepti
43	11	100.0	40	19	AAW47232		Beta-amyloid pepti
44	11	100.0	40	19	AAW47226		Beta-amyloid pepti
45	11	100.0	40	22	AAE05483		Human peptide anti

ALIGNMENTS

RESULT 1
AA60369
ID AAR60369 standard; peptide; 11 AA.
XX
AC AAR60369;
XX
DT 15-MAR-1995 (first entry)
XX
DE Beta-amyloid (25-35).
XX
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
XX
OS Homo sapiens.
XX
PN WO9417197-A.
XX
PD 04-AUG-1994.
XX
PF 24-JAN-1994; 94WO-JP00089.
XX
PR 25-JAN-1993; 93JP-0010132.
PR 05-FEB-1993; 93JP-0019035.
PR 16-NOV-1993; 93JP-0286985.
PR 28-DEC-1993; 93JP-0334773.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kitada C, Odaka A, Suzuki N;
XX
DR WPI; 1994-264110/32.
XX
PT Antibodies recognising specific parts of beta-amyloid - can be
used for diagnosis of diseases implicating beta-amyloid, such as

PT Alzheimer's disease

PS Claim 2; Page 84; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgaiiglm 11

RESULT 2

AAR87948

ID AAR87948 standard; peptide; 11 AA.

XX AAR87948;

XX DT 05-MAR-1996 (first entry)

XX DE beta-amyloid (25-35) peptide.

XX KW Alzheimer's disease; beta-amyloid; plaque; glycosaminoglycan;

XX KW proteoglycan; A-beta.

XX OS Synthetic.

XX PN WO9506477-A1.

XX PD 09-MAR-1995.

XX PF 29-AUG-1994; 94WO-US09853.

XX PR 31-AUG-1993; 93US-0114942.

XX PA (GLIA-) GLIATECH INC.

XX PI Brunden KR, Frederickson RCA, Gupta-Bansal R, Richtercook NJ;

XX WPI; 1995-115259/15.

XX PT Treating Alzheimer's disease by using cpds. that inhibit beta

XX PT amyloid binding - to glycosaminoglycan(s)

XX PS Claim 49; Page 64; 88pp; English.

XX CC The invention relates to new chemical compounds which are peptides of formulae XXNX (I), XXNX2 (II) and XXNX2X3 (III), and peptides comprising the sequences (I), (II) or (III) and containing not greater than 8 amino acid residues. In the formulae, X is any amino acid with a cationic side chain, N and Z are neutral amino acids, and two of X1, X2 and X3 are amino acids with an anionic side chain and the third is an amino acid with an anionic or neutral side chain. Also new is the peptide Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is the latter undecapeptide which represents amino acids 25-35 of the beta-amyloid peptide A-beta.

XX CC The peptides inhibit the binding of glycosaminoglycans and/or proteoglycans to A-beta peptide and hence can be used for preventing the formation of amyloid plaques and for treating Alzheimer's disease.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 16; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgaiiglm 11

RESULT 3

AAR92807

ID AAR92807 standard; peptide; 11 AA.

XX AAR92807;

XX DT 18-OCT-1996 (first entry)

XX DE Human beta-amyloid 25-35.

XX KW PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's disease;

XX KW Down's syndrome; inhibition; neurotoxicity; beta-amyloid 25-35.

XX OS Homo sapiens.

XX PN WO9607425-A1.

XX PD 14-MAR-1996.

XX PF 07-SEP-1995; 95WO-US10989.

XX PR 09-SEP-1994; 94US-0306872.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Perlmutter DH;

XX WPI; 1996-171392/17.

XX PT Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor - used for inhibiting amyloid-beta protein neurotoxicity in e.g. Alzheimer's disease

XX PS Claim 5; Page 18; 31pp; English.

XX CC The peptides PB145, PB446 and PB96 can be used to inhibit the neurotoxicity of the present peptide, beta-amyloid 25-35, and are therefore useful in the treatment of Alzheimer's disease and Down's syndrome.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgaiiglm 11

RESULT 4

AAW23336

ID AAW23336 standard; peptide; 11 AA.

XX AAW23336;

XX DT 12-MAR-1998 (first entry)

XX DE Amyloid beta peptide 2 used to inhibit damage to cells in Alzheimer's.

XX SQ Sequence 11 AA;

KW Amyloid beta peptide; extracellular deposit; Alzheimer's disease;
 KW neurite outgrowth; microglial activation; neuronal cell degeneration;
 KW receptor for advanced glycosylation end product;
 KW amyloid beta peptide fibril.
 XX
 OS Homo sapiens.
 XX
 PN WO9726913-A1.
 XX
 PD 31-JUL-1997.
 XX
 PF 21-JAN-1997; 97WO-US00857.
 XX
 PR 26-JAN-1996; 96US-0592070.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Schmidt AM, Stern D, Yan SD;
 DR WPI; 1997-393374/36.
 XX
 XX Inhibiting damage to cells in e.g. Alzheimer's disease - using an
 PT agent which inhibits interaction of an amyloid-beta peptide with a
 PT receptor for advanced glycosylation end product
 XX
 PS Claim 5; Page 10; 91pp; English.
 XX
 CC Peptides AAW23335-36 are portions of the the amyloid beta peptide, which
 CC is the principal component of extracellular deposits in Alzheimer's
 CC disease. It has been shown to promote neurite outgrowth, generate
 CC reactive oxygen intermediates, induce cellular oxidant stress, lead to
 CC neuronal cytotoxicity, and promote microglial activation. The present
 CC peptide, which comprises amino acids 25-35 of the amyloid beta peptide,
 CC is used in a pharmaceutical composition. This composition comprises an
 CC agent capable of inhibiting interaction of an amyloid-beta peptide with
 CC a receptor for advanced glycosylation end product and a carrier. A
 CC method for inhibiting interaction of amyloid beta peptide with a receptor
 CC for advanced glycosylation on the surface of a cell comprises contacting
 CC the cell with e.g. present peptide. Depending on the type of cell,
 CC inhibiting the interaction between the amyloid beta peptide and the
 CC receptor for advanced glycosylation can be used for inhibiting
 CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta
 CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid
 CC beta peptide into a fibril, inhibiting aggregation of amyloid beta
 CC peptide on the surface of a cell, inhibiting infiltration of a microglial
 CC cell into senile plaques, and inhibiting activation of microglial cells
 CC by amyloid beta peptide. The methods can be used for treating e.g.
 CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic
 CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia
 CC associated with head trauma, amyotrophic lateral sclerosis, multiple
 CC sclerosis or neuronal degeneration.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 11; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGAIIGLM 11
 Db 1 gsnkgaiiglm 11
 RESULT 5
 AAW64497
 ID AAW64497 standard; peptide; 11 AA.
 XX
 AC AAW64497;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Neurotoxic beta-amyloid peptide decoy peptide #10.

XX
 KW Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
 KW aggregate; Alzheimers disease; decoy; treatment.
 XX
 OS Synthetic.
 XX
 PN WO9830229-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 09-JAN-1998; 98WO-US00653.
 XX
 PR 29-OCT-1997; 97US-0960188.
 PR 10-JAN-1997; 97US-0035847.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Blanchard BJ, Ingram VM;
 DR WPI; 1998-398795/34.
 XX
 XX Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor,
 PT useful for, e.g. treating Alzheimer's disease
 XX
 PS Example 4; Page 42; 68pp; English.
 XX
 CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
 CC form aggregates that increase calcium influx into neuronal cells. Such
 CC peptides can be used in the treatment of diseases associated with
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
 CC injection and orally, or from slow-release implants.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 11; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGAIIGLM 11
 Db 1 gsnkgaiiglm 11
 RESULT 6
 AAW47231
 ID AAW47231 standard; peptide; 11 AA.
 XX
 AC AAW47231;
 XX
 DT 22-MAY-1998 (first entry)
 XX
 DE Beta-amyloid peptide residues 25-35.
 KW Screening assay; beta-amyloid peptide; treatment;
 KW amyloidosis disease; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN US5721106-A.
 XX
 PD 24-FEB-1998.
 XX
 PF 12-SEP-1994; 94US-0304585.
 PR 12-SEP-1994; 94US-0304585.
 PR 13-AUG-1991; 91US-0744767.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (MINU) UNIV MINNESOTA.

XX Maggio JE, Mantyh PW;
 XX WPI; 1998-168404/15.
 XX New in vitro screening assay for Alzheimer's disease drugs -
 PT comprises assessing binding of labelled beta-amyloid peptide to silk
 PT sample
 XX Example 1; Columns 29-30; 36pp; English.
 XX The present sequence was used in the development of a novel in
 CC vitro screening assay for agents capable of affecting the
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method
 CC comprises contacting a silk sample with labelled BAP, optionally
 CC in the presence of a test agent, detecting the amount of label
 CC bound to the silk and assessing the effect of the agent on the
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are
 CC potentially useful for treating amyloidosis diseases, especially
 CC Alzheimer's disease.
 XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 Db 1 gsnkgaiiglm 11
 |||||

RESULT 7
 AAW81470
 ID AAW81470 standard; peptide; 11 AA.
 XX AAW81470;
 XX 28-JAN-1999 (first entry)
 DE Synthetic amyloid beta (Abeta) peptide 5 (residues 25-35).
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.
 XX Synthetic.
 OS US5840838-A.
 PN 24-NOV-1998.
 XX 29-FEB-1996; 96US-0609090.
 XX 29-FEB-1996; 96US-0609090.
 PR (KENT) UNIV KENTUCKY RES FOUND.
 PA Aksenov M, Butterfield DA, Carney JM, Hensley K;
 PI WPI; 1999-034120/03.
 DR Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity
 PS Claim 5; Columns 9-10; 14pp; English.
 XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the

CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide -enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.
 XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 Db 1 gsnkgaiiglm 11
 |||||

RESULT 8
 AAY52133
 ID AAY52133 standard; peptide; 11 AA.
 XX AAY52133;
 XX 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #2.
 KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.
 XX Homo sapiens.

OS WO9954485-A1.
 PN 28-OCT-1999.
 PD 16-APR-1999; 99WO-US08427.
 PF 17-APR-1998; 98US-0062365.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA Schmidt AM, Stern D;
 PI WPI; 2000-013260/01.
 DR Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -
 XX Claim 28; Page 62; 88pp; English.

XX This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 1 gsnkgaiiglm 11

RESULT 9
AAB91775
ID AAB91775 standard; Peptide; 11 AA.

XX AC AAB91775;

XX DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:951.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 504; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 1 gsnkgaiiglm 11

RESULT 10

AAB91808

ID AAB91808 standard; Peptide; 11 AA.

XX AC AAB91808;

XX DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:984.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 516; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 1 gsnkgaiiglm 11

RESULT 11
 AAW64498
 ID AAW64498 standard; peptide; 14 AA.
 XX
 AC AAW64498;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Neurotoxic beta-amyloid peptide decoy peptide #11.
 XX
 KW Beta-amyloid peptide; beta-AP; neurotoxin; calcium influx;
 KW aggregate; Alzheimers disease; decoy; treatment.
 XX
 OS Synthetic.
 XX
 PN WO9830229-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 09-JAN-1998; 98WO-US00053.
 XX
 PR 29-OCT-1997; 97US-0960188.
 PR 10-JAN-1997; 97US-0035847.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Blanchard BJ, Ingram VM;
 XX
 DR WPI; 1998-398795/34.
 XX
 PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by
 PT administering decoy peptide or other calcium-influx inhibitor,
 PT useful for, e.g. treating Alzheimer's disease
 XX
 PS Example 4; Page 43; 68pp; English.
 XX
 CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
 CC form aggregates that increase calcium influx into neuronal cells. Such
 CC peptides can be used in the treatment of diseases associated with
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
 CC injection and orally, or from slow-release implants.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 11; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGAIIGLM 11
 Db | | | | | | | | | |
 4 gsnkgailglm 14
 RESULT 12
 AAB91782
 ID AAB91782 standard; Peptide; 14 AA.
 XX
 AC AAB91782;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:958.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.

XX WO200069900-A2.
 PN
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 XX
 PS Disclosure: Page 507; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body;
 CC modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 11; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGAIIGLM 11
 Db | | | | | | | | | |
 4 gsnkgailglm 14
 RESULT 13
 AAB91788
 ID AAB91788 standard; Peptide; 14 AA.
 XX
 AC AAB91788;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:964.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 XX
 PS Disclosure; Page 509; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 11; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 DB 4 gsnkgaiiglm 14
 |||||

RESULT 14
 AAB91815
 ID AAB91815 standard; Peptide; 14 AA.
 XX
 AC AAB91815;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:991.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 PR 10-SEP-1999; 99US-0134406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.

PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 XX
 PS Disclosure; Page 519; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 11; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 DB 4 gsnkgaiiglm 14
 |||||

RESULT 15
 AAB91805
 ID AAB91805 standard; Peptide; 24 AA.
 XX
 AC AAB91805;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:981.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI WPI; 2001-112059/12.
XX
DR
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
XX
PS Disclosure; Page 515; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxy/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 11; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSNKGAIIGLM 11
Db 9 gsnkgailglm 19
|||||

Search completed: April 24, 2002, 09:21:50
Job time: 249 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:22:29 ; Search time 32.21 Seconds
(without alignments)
7.685 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 11
Sequence: 1 GSNKGAIIGLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 21252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pap.*
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	11	100.0	11	1 US-07-744-767A-3	Sequence 3, Appli
2	11	100.0	11	1 US-08-306-872-2	Sequence 2, Appli
3	11	100.0	11	1 US-08-346-849-5	Sequence 5, Appli
4	11	100.0	11	1 US-08-304-585-3	Sequence 3, Appli
5	11	100.0	11	1 US-08-302-808-8	Sequence 8, Appli
6	11	100.0	11	2 US-08-433-734-3	Sequence 3, Appli
7	11	100.0	11	2 US-08-609-090-5	Sequence 5, Appli
8	11	100.0	11	2 US-08-986-948-8	Sequence 8, Appli
9	11	100.0	11	2 US-08-293-284-5	Sequence 5, Appli
10	11	100.0	11	4 US-09-005-215-10	Sequence 10, Appli
11	11	100.0	11	5 PCT-US95-10989-2	Sequence 2, Appli
12	11	100.0	14	4 US-09-005-215-11	Sequence 11, Appli
13	11	100.0	26	1 US-08-304-585-7	Sequence 7, Appli
14	11	100.0	34	2 US-08-475-579A-4	Sequence 4, Appli
15	11	100.0	35	1 US-08-304-585-6	Sequence 6, Appli
16	11	100.0	35	2 US-08-612-785B-16	Sequence 16, Appli
17	11	100.0	35	2 US-08-612-785B-36	Sequence 36, Appli
18	11	100.0	35	2 US-08-612-785B-39	Sequence 39, Appli
19	11	100.0	35	2 US-08-612-785B-40	Sequence 40, Appli
20	11	100.0	36	2 US-08-609-090-6	Sequence 6, Appli
21	11	100.0	38	1 US-08-302-808-1	Sequence 1, Appli
22	11	100.0	38	2 US-07-737-371E-68	Sequence 68, Appli
23	11	100.0	38	2 US-08-986-948-1	Sequence 1, Appli
24	11	100.0	39	1 US-08-304-585-5	Sequence 5, Appli
25	11	100.0	39	1 US-08-302-808-2	Sequence 2, Appli
26	11	100.0	39	2 US-08-609-090-7	Sequence 7, Appli
27	11	100.0	39	2 US-08-682-245A-1	Sequence 1, Appli

28	11	100.0	39	2 US-08-986-948-2	Sequence 2, Appli
29	11	100.0	40	1 US-07-744-767A-1	Sequence 1, Appli
30	11	100.0	40	1 US-08-235-400-2	Sequence 2, Appli
31	11	100.0	40	1 US-08-476-464A-2	Sequence 2, Appli
32	11	100.0	40	1 US-08-304-585-1	Sequence 1, Appli
33	11	100.0	40	1 US-08-304-585-8	Sequence 8, Appli
34	11	100.0	40	1 US-08-302-808-3	Sequence 3, Appli
35	11	100.0	40	2 US-08-433-734-1	Sequence 1, Appli
36	11	100.0	40	2 US-08-609-090-8	Sequence 8, Appli
37	11	100.0	40	2 US-07-737-371E-69	Sequence 69, Appli
38	11	100.0	40	2 US-08-682-245A-2	Sequence 2, Appli
39	11	100.0	40	2 US-08-986-948-3	Sequence 3, Appli
40	11	100.0	40	2 US-08-461-216-1	Sequence 1, Appli
41	11	100.0	40	4 US-08-959-148-1	Sequence 1, Appli
42	11	100.0	40	5 PCT-US92-06700-1	Sequence 1, Appli
43	11	100.0	41	1 US-07-819-361-1	Sequence 1, Appli
44	11	100.0	41	1 US-08-302-808-4	Sequence 4, Appli
45	11	100.0	41	2 US-08-682-245A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-07-744-767A-3
; Sequence 3, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600,226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-744-767A-3

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSNKGAIIGLM 11
DB 1 GSNKGAIIGLM 11

RESULT 2
US-08-872-2
; Sequence 2, Application US/08306872
; Patent No. 5514653
; GENERAL INFORMATION:
; APPLICANT: Perlmutter, David H.
; TITLE OF INVENTION: Method of Blocking the SEC Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,872
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2833
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-306-872-2

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
Db 1 GSNKGAIIGLM 11

RESULT 3
US-08-346-849-5
; Sequence 5, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-346-849-5

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
Db 1 GSNKGAIIGLM 11

RESULT 4
US-08-304-585-3
; Sequence 3, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyn, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
US-08-304-585-3

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 5

US-08-302-808-8
; Sequence 8, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302.808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MEDIUM TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-8

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 6

US-08-433-734-3
; Sequence 3, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-734-3

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 7

US-08-609-090-5
; Sequence 5, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
US-08-609-090-5

ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-5

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 8
US-08-986-948-8
Sequence 8, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-8

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 9
US-08-293-284A-5
Sequence 5, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-5

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 10

US-09-005-215-10
Sequence 10, Application US/09005215
Patent No. 6172043

GENERAL INFORMATION:
APPLICANT: Ingram, Vernon M.

APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S

TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

STREET: 600 ATLANTIC AVENUE
CITY: BOSTON

STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA

ZIP: 02210
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847

FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.

REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0656/7035

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
US-09-005-215-10

Query Match 100.0%; Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 11

PCT-US95-10989-2

Sequence 2, Application PC/TUS9510989
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Method of Blocking the SEC Receptor

NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10989

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,872

FILING DATE: 09-SEP-1994
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US95-10989-2

Query Match

Best Local Similarity 100.0%; Score 11; DB 5; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
DB 1 GSNKGAIIGLM 11

RESULT 12

US-09-005-215-11

Sequence 11, Application US/09005215
Patent No. 6172043

GENERAL INFORMATION:
APPLICANT: Ingram, Vernon M.

APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S

TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

STREET: 600 ATLANTIC AVENUE
CITY: BOSTON

STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA

ZIP: 02210
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215

FILING DATE:
CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/035,847
;; FILING DATE: 10-JAN-1997
;; PRIOR APPLICATION NUMBER: 08/960,188
;; FILING DATE: 29-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gates, Edward R.
;; REGISTRATION NUMBER: 31,616
;; REFERENCE/DOCKET NUMBER: M0656/7035
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-720-3500
;; TELEFAX: 617-720-2441
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
US-09-005-215-11

Query Match 100.0%; Score 11; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 4 GSNKGAIIGLM 14

RESULT 13
US-08-304-585-7
;; Sequence 7, Application US/08304585
;; Patent No. 5721106
;; GENERAL INFORMATION:
;; APPLICANT: Maggio, John E.
;; APPLICANT: Mantyh, Patrick W.
;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
;; METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
;; STREET: P.O. Box 581415
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55458-1415
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/304,585
;; FILING DATE: 12-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Muetting, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 110.00010120
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-305-1217
;; TELEFAX: 612-305-1228
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide

US-08-304-585-7

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 16 GSNKGAIIGLM 26

RESULT 14
US-08-475-579A-4
;; Sequence 4, Application US/08475579A
;; Patent No. 5854215
;; GENERAL INFORMATION:
;; APPLICANT: Mark A. Findels et al.
;; TITLE OF INVENTION: Modulators of [SYMBOL 98 \f "symbol"]-Amyloid Peptide Aggre
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,579A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/404,831
;; FILING DATE: 14-MAR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kara, Catherine J.
;; REGISTRATION NUMBER: P41,106
;; REFERENCE/DOCKET NUMBER: PPI-002CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
US-08-475-579A-4

Query Match 100.0%; Score 11; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 19 GSNKGAIIGLM 29

RESULT 15
US-08-304-585-6
;; Sequence 6, Application US/08304585
;; Patent No. 5721106
;; GENERAL INFORMATION:
;; APPLICANT: Maggio, John E.
;; APPLICANT: Mantyh, Patrick W.

;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
;; STREET: P.O. Box 581415
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55458-1415
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/304,585
;; FILING DATE: 12-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mueiting, And M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 110.00010120
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-305-1217
;; TELEFAX: 612-305-1228
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;;
US-08-304-585-6

Query Match 100.0%; Score 11; DB 1; Length 35;
Best Local Similarity 100.0%; Pred.No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
|||||
Db 25 GSNKGAIIGLM 35

Search completed: April 24, 2002, 09:22:29
Job time: 248 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:15 ; Search time 38.65 Seconds
(without alignments)
21.680 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 11

Sequence: 1 GSNKGAIITGLM 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174592 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	42	2	PN0512
2	11	100.0	57	2	E60045
3	11	100.0	57	2	F60045
4	11	100.0	57	2	B60045
5	11	100.0	57	2	D60045
6	11	100.0	57	2	A60045
7	11	100.0	57	2	B60045
8	11	100.0	82	2	P00438
9	11	100.0	695	1	A49795
10	11	100.0	695	1	A27485
11	11	100.0	695	2	S00550
12	11	100.0	747	2	JH0773
13	11	100.0	770	1	ORH044
14	7	63.6	247	2	B83880
15	6	54.5	130	2	S63533
16	6	54.5	176	2	B83837
17	6	54.5	184	1	A30128
18	6	54.5	192	2	T22142
19	6	54.5	205	2	F72422
20	6	54.5	205	2	G82358
21	6	54.5	219	2	I52644
22	6	54.5	230	2	B82456
23	6	54.5	234	2	E70982
24	6	54.5	266	2	T10609
25	6	54.5	290	2	E86284
26	6	54.5	292	1	A39871
27	6	54.5	297	1	S31484
28	6	54.5	297	1	S31486
29	6	54.5	297	1	JN0773

30	6	54.5	297	2	JC4500	basic calponin - h
31	6	54.5	297	2	G02142	smooth muscle cell
32	6	54.5	297	2	F82214	galactoside ABC tr
33	6	54.5	339	2	S32624	INDC1 protein - f
34	6	54.5	358	2	T02903	hypothetical prote
35	6	54.5	382	2	G85234	hypothetical prote
36	6	54.5	428	1	A42971	cytochrome P450ter
37	6	54.5	442	1	S36204	probable beta-keto
38	6	54.5	449	2	T44643	galactosyl transfe
39	6	54.5	450	2	E70590	3-phosphoshikimate
40	6	54.5	462	2	T34365	hypothetical prote
41	6	54.5	468	2	T10595	hypothetical prote
42	6	54.5	512	2	S28663	cytochrome-c oxida
43	6	54.5	541	1	MMBYH2	glucose transport
44	6	54.5	546	2	S48313	hexose transport p
45	6	54.5	636	2	C83724	PTS system, beta-9

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A:Reference number: PN0512; MWID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SH1>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 11; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIITGLM 11
DB 25 GSNKGAIITGLM 35

RESULT 2

E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MWID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 11; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIITGLM 11
DB 30 GSNKGAIITGLM 40

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 30 GSNKGATIGLM 40

RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 30 GSNKGATIGLM 40

RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 30 GSNKGATIGLM 40

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 30 GSNKGATIGLM 40

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 30 GSNKGATIGLM 40

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MID:93075180

A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAY>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 11; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11
|||||
Db 41 GSNKGAIIIGLM 51

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a F
A:Reference number: A49795; MUID:91273117
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 11; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11
|||||
Db 621 GSNKGAIIIGLM 631

RESULT 10
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A:Reference number: A27485; MUID:88106489
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458

A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Kizumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheim
A:Reference number: I49485; MUID:92209998
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RRS>
A:Cross-references: GB:D10603; NID:9220328; PIDN:BAAO1456.1; PID:9220329
C:Genetics:
A:Map position: 16c3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 11; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11
|||||
Db 621 GSNKGAIIIGLM 631

RESULT 11
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Halblach, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
A:Reference number: S00550; MUID:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617
R:Schubert, D.; Schroeder, R.; Lacordiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 11; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 621 GSNKGATIGLM 631

RESULT 12
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:q263150; PIDN:AAB24853.1; PID:q263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 11; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 673 GSNKGATIGLM 683

RESULT 13
ORHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIIa inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A32260; A35466; I39452; I39451; I39453; I59562; A44
4688; A28583; A29302; A60805; J10038; S06121; A60355; A5011; A38384; S29076; S38255; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360
A:Note: alternative splice form APP(695)
R:Ja Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:q516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865
R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:q178616
A:Accession: I39451
A:Molecule type: DNA
A:Residues: 1-530, 'QWMPVPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615
R:Yoshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Accession: I39453
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
A:Note: a mutation with 693-Gln is presented
R:Wurrell, J.; Farlow, M.; Chetli, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:q236721
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93055397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:q257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:q257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
Nature 325, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-References: GB:Y00264; NID:928525; PIDN:CAA6374.1; PID:928526
 A:Note: alternative splice form APP(695)
 R:Robkiss, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-References: GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:9178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-References: GB:M15533; NID:9178706; PIDN:AAA35540.1; PID:9178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TRAN1>
 A:Cross-References: GB:M15532; NID:917957; PIDN:AAA51564.1; PID:917958
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-References: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-References: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-References: NID:928816; PIDN:CAA30041.1; PID:9292611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
 A:Reference number: A30320

A:Accession: A30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-References: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 11; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGATIGLM 11
 |||||
 Db 696 GSNKGATIGLM 706
 RESULT 14
 B3880
 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [imported] - Bacillus halodurans (s
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: B83880
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20263314
 A:Accession: B83880
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-247 <STO>
 A:Cross-References: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA805561.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1842
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 Query Match 63.6%; Score 7; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KGATIGL 10
 |||||
 Db 159 KGATIGL 165
 RESULT 15
 S63533
 Profilin basic isoform - Entamoeba histolytica
 C:Species: Entamoeba histolytica
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S63533; S63474
 R:Binder, M.; Ortnier, S.; Erben, H.; Scheiner, O.; Wiedermann, G.; Valenta, R.; Duch
 Eur. J. Biochem. 233, 976-981, 1995
 A>Title: The basic isoform of profilin in pathogenic Entamoeba histolytica: cDNA clon

A:Reference number: S63474; MUID:96085166
A:Accession: S63533
A:Molecule type: mRNA
A:Residues: 1-130 <BIN>
A:Cross-references: EMBL:X90911; NID:g1070154; PID:g1070155
A:Accession: S63474
A:Molecule type: protein
A:Residues: 74-84;86-94 <BIW>
C:Superfamily: profilin
C:Keywords: actin binding

Query Match 54.5%; Score 6; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GAIIGL 10
|||||
DB 20 GAIIGL 25

Search completed: April 24, 2002, 09:23:16
Job time: 245 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:53 ; Search time 21.46 Seconds

(without alignments)
18.794 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 11
Sequence: 1 GSNKGATIGLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	11	100.0	A4_PIG	Q29023 sus scrofa
2	11	100.0	A4_URSWA	Q29149 ursus marit
3	11	100.0	A4_CANFA	Q28280 canis fam1
4	11	100.0	A4_RABIT	Q28748 oryctolagus
5	11	100.0	A4_SHEEP	Q28757 ovis aries
6	11	100.0	A4_BOVIN	Q28053 bos taurus
7	11	100.0	A4_SAISC	Q95241 salmirl sci
8	11	100.0	A4_HUMAN	P05067 homo sapien
9	11	100.0	A4_MOUSE	P12023 mus musculu
10	11	100.0	A4_RAT	P08592 rattus norv
11	100.0	770	A4_RAT	P49330 entamoeba h
12	6	54.5	MP20_DROME	P14318 drosophila
13	6	54.5	NP25_MOUSE	Q91498 mus musculu
14	6	54.5	NP25_MOUSE	Q52946 rhizobium m
15	6	54.5	NP25_MOUSE	Q52946 rhizobium m
16	6	54.5	NP25_MOUSE	Q52946 rhizobium m
17	6	54.5	NP25_MOUSE	Q52946 rhizobium m
18	6	54.5	NP25_MOUSE	Q52946 rhizobium m
19	6	54.5	NP25_MOUSE	Q52946 rhizobium m
20	6	54.5	NP25_MOUSE	Q52946 rhizobium m
21	6	54.5	NP25_MOUSE	Q52946 rhizobium m
22	6	54.5	NP25_MOUSE	Q52946 rhizobium m
23	6	54.5	NP25_MOUSE	Q52946 rhizobium m
24	6	54.5	NP25_MOUSE	Q52946 rhizobium m
25	6	54.5	NP25_MOUSE	Q52946 rhizobium m
26	6	54.5	NP25_MOUSE	Q52946 rhizobium m
27	6	54.5	NP25_MOUSE	Q52946 rhizobium m
28	6	54.5	NP25_MOUSE	Q52946 rhizobium m
29	6	54.5	NP25_MOUSE	Q52946 rhizobium m
30	6	54.5	NP25_MOUSE	Q52946 rhizobium m
31	6	54.5	NP25_MOUSE	Q52946 rhizobium m
32	6	54.5	NP25_MOUSE	Q52946 rhizobium m
33	6	54.5	NP25_MOUSE	Q52946 rhizobium m

34	6	54.5	661	1	RDGC_DROME	P40421 drosophila
35	6	54.5	764	1	SYPR_HELPU	092f8 helicobacte
36	6	54.5	813	1	GYRA_TREPA	083051 treponema p
37	6	54.5	837	1	NCM2_MOUSE	035136 mus musculu
38	5	45.5	47	1	RK2_WHEAT	P15344 triticum ae
39	5	45.5	50	1	VG38_BPM15	005248 mycobacteri
40	5	45.5	60	1	YH05_VACCV	P17356 vaccinia v1
41	5	45.5	89	1	RS16_MYCGE	P47684 mycoplasma
42	5	45.5	114	1	PFDE_SCHPO	014450 schizosacch
43	5	45.5	125	1	RSBE_ARCFU	028130 archaeeoglob
44	5	45.5	126	1	RL26_SCHPO	P78946 schizosacch
45	5	45.5	127	1	RSBE_PYRHO	058830 pyrococcus

ALIGNMENTS

```

RESULT 1
A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTRAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL: X56127; CAA39592.1; -
CC DR HSSP: P05067; 1AHL.
CC DR InterPro: IPR001868; A4_APP.
CC DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE: PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT CHAIN 1 1
CC FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
CC FT NON_TER 57 57 POTENTIAL.
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
Query Match 100.0%; Score 11; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GSNKGATIGLM 11

```

Db 30 GSNKGAIIGLM 40

RESULT 2

AC_URSMA STANDARD; PRT; 57 AA.

ID A4_URSMA

AC Q29149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Ursus maritimus (Polar bear) (Thalarcos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -1 FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1 SIMILARITY: BELONGS TO THE APP FAMILY.

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CC

DR EMBL: X56128; CAA39593.1; -

DR HSSP: P05067; IAML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

SO

QY 1 GSNKGAIIGLM 11

Db 30 GSNKGAIIGLM 40

RESULT 3

ID A4_CANFA STANDARD; PRT; 58 AA.

AC Q28280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

RT

GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -1 FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1 SIMILARITY: BELONGS TO THE APP FAMILY.

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CC

DR EMBL: X56125; CAA39590.1; -

DR HSSP: P05067; IAML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON_TER 58 58

FT SEQUENCE 58 AA; 6285 MW; 8469DA88A2E12DFA CRC64;

SO

QY 1 GSNKGAIIGLM 11

Db 31 GSNKGAIIGLM 41

RESULT 4

ID A4_RABIT STANDARD; PRT; 58 AA.

AC Q28748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis."

RT

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6
FT DOMAIN <1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 57 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

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Query Match      100.0%; Score 11; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GSNKGAIITGLM 11
   |||||
Db 30 GSNKGAIITGLM 40

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RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6
FT DOMAIN <1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 57 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

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Query Match      100.0%; Score 11; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GSNKGAIITGLM 11
   |||||
Db 30 GSNKGAIITGLM 40

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RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

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FT  NON_TER      1      1
FT  CHAIN         7      49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT  DOMAIN        <1      34      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM      35      58      POTENTIAL.
FT  DOMAIN        59      >59      CYTOPLASMIC (POTENTIAL).
FT  NON_TER      59      59
SQ  SEQUENCE      59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match      100.0%; Score 11; DB 1; Length 59;
Best Local Similarity 100.0%; Pred No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GSNKGATIGLM 11
    |||||
Db  31 GSNKGATIGLM 41

RESULT 7
A4_SAISC      STANDARD;      PRT;      751 AA.
AC  095241;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE  AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP.
OS  Saimiri sciureus (Common squirrel monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX  NCBI_TaxID=9521;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver and Kidney;
RX  MEDLINE=96108492; PubMed=8532114;
RA  Levy E., Amorim A., Frangione B., Walker L.C.;
RT  "beta-amyloid precursor protein gene in squirrel monkeys with
RL  cerebral amyloid angiopathy.";
CC  Neurobiol. Aging 16:805-808(1995).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O).
CC  -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC  -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC  PHOSPHORYLATION (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL; S81024; AAD14347.1; -
DR  InterPro; IPR001868; A4_APP.
DR  InterPro; IPR002223; Kunitz_BPTI.
DR  Pfam; PF02177; A4_EXTRA; 1.
DR  Pfam; PRO0014; Kunitz_BPTI; 1.
DR  PRINTS; PRO0203; AMYLOIDA4.
DR  PRINTS; PRO0204; BETAAMYLOID.
DR  PRINTS; PRO0759; BASICPTASE.
DR  SMART; SM00006; A4_EXTRA; 1.
DR  SMART; SM00131; KU; 1.
DR  PROSITE; PS00319; A4_EXTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
DR  PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR  PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW  Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW  Signal; Serine protease inhibitor.
FT  SIGNAL        1      17      BY SIMILARITY.
FT  CHAIN         18      751      A4 PROTEIN.
FT  CHAIN         653      695      BETA-AMYLOID PROTEIN (POTENTIAL).
FT  DOMAIN        18      680      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM      681      704      POTENTIAL.
FT  DOMAIN        705      751      CYTOPLASMIC (POTENTIAL).
FT  DOMAIN        287      345      BPTI/KUNITZ INHIBITOR.
FT  SITE          740      743      CLATHRIN-BINDING (BY SIMILARITY).
FT  ACT_SITE      301      302      REACTIVE BOND.
FT  DISULFID      291      341      BY SIMILARITY.
FT  DISULFID      300      324      BY SIMILARITY.
FT  DISULFID      316      337      BY SIMILARITY.
FT  CARBOHYD      523      523      N-LINKED (GLCNAC... ) (PROBABLE).
FT  CARBOHYD      552      552      N-LINKED (GLCNAC... ) (PROBABLE).
SQ  SEQUENCE      751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match      100.0%; Score 11; DB 1; Length 751;
Best Local Similarity 100.0%; Pred No. 9.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GSNKGATIGLM 11
    |||||
Db  677 GSNKGATIGLM 687

RESULT 8
A4_HUMAN      STANDARD;      PRT;      770 AA.
AC  P05067; P09000; 016011;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
DE  (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP OR A4 OR CVAP OR ADL.
OS  Homo sapiens (human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=87144572; PubMed=2881207;
RA  Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RT  Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT  "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RL  cell-surface receptor.";
RL  Nature 325:733-736(1987).
RN  [2]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=88122639; PubMed=2893289;
RX  Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RA  Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA  Cordell B.;
RT  "A new A4 amyloid mRNA contains a domain homologous to serine
RT  proteinase inhibitors.";
RL  Nature 331:525-527(1988).
RN  [3]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=89128427; PubMed=2783775;
RA  Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA  Unterbeck A.G., Beyreuther K., Mueller-Hill B.;
RT  "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT  is encoded by 16 exons.";
RL  Nucleic Acids Res. 17:517-522(1989).
RN  [4]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=97263807; PubMed=9108164;
RA  Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,

```

RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE-88122640; PubMed-2893290;
 RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE-88122641; PubMed-2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-533(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-370 FROM N.A.
 RX MEDLINE-87231971; PubMed-3035574;
 RA Kobakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE-88124954; PubMed-2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE-88035004; PubMed-3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE-9036318; PubMed-2110105;
 RA Yoshikawa S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX TISSUE-Liver;
 RC MEDLINE-89016647; PubMed-3140222;
 RA Schon E.A., Mitra S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE-87250462; PubMed-3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE-89384866; PubMed-2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RX Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE-90211252; PubMed-1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE-93188965; PubMed-8446172;
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE-99215582; PubMed-10201399;
 RA Rosjohn J., Cappai R., Fell S.C., Henry A., McKinstrey W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE-91104913; PubMed-2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossakof A.A.;
 RT "ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 39:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE-92031488; PubMed-1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayley R.M.,
 RA Kamack M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-94281210; PubMed-7516706;
 RA Talarious J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE-97128622; PubMed-8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE-98359783; PubMed-9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-20400066; PubMed-10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE-88296437; PubMed-2900137;

RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RL EMBO J. 7:949-957(1988).
 RN [24]
 RP REVIEW.
 RX MEDLINE=92271194; PubMed=1589757;
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective.";
 RL Science 256:780-783(1992).
 RN [25]

Query Match 100.0%; Score 11; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIGLM 11
 DB 696 GSNKGAIGLM 706

RESULT 9
 A4_MOUSE STANDARD; PRT; 770 AA.
 ID A4_MOUSE
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Bergh H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-Placenta;
 RX MEDLINE=89345111; PubMed=2556710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domestica.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X59379; -; NOT_ANNOTATED_CDS.
 CC EMBL: M18373; AAA37139.1; -;
 CC EMBL: X15210; CAA33280.1; -;
 CC EMBL: D10603; BAA01456.1; -;
 CC EMBL: M24397; AAA38929.1; -;
 CC PIR: A27485; A27485.
 CC PIR: S04855; S04855.
 CC PIR: S19727; S19727.
 CC MGD: MGI:88059; APP.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOID4.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC PRINTS: PR00759; BASICPTASE.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 CC GlycoProtNet: Amyloid; Neurone; Transmembrane; Signal;
 CC Alternative splicing; Serine
 CC protease inhibitor.
 CC BY SIMILARITY.
 CC CHAIN 1 17
 CC 18 770
 CC -----
 CC HOMOLOG.
 CC ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 CC -----
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC EQUIVALENT OF BETA-AMYLOID PROTEIN.
 CC BPTI/KUNITZ INHIBITOR.
 CC CLATHRIN-BINDING (BY SIMILARITY).
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC E -> V (IN ISOFORM APP(695)).
 CC MISSING (IN ISOFORM APP(695)).
 CC MISSING (IN ISOFORM APP(751)).
 CC MISSING (IN ISOFORM APP(751)).
 CC SEQUENCE 770 AA; 86752 MW; 26C50DB0890CA7A CRC64;

Query Match 100.0%; Score 11; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
 |||||||||
 DB 696 GSNKGATIGLM 706

RESULT 10
 A4_RAT STANDARD: PRT: 770 AA.
 ID A4_RAT
 AC P08592;
 DT 01-AUG-1988 (rel. 08, Created)
 DT 01-DEC-1992 (rel. 24, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=8812583; PubMed=2900758;
 RA Shivers B.D., Hildich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat pre4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X07648; CAA30488.1; -
 CC EMBL: X14066; CAA32229.1; -
 CC PIR: S00550; S00550.
 CC PIR: S03607; S03607.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRINTS: PR00204; BETAMAMLOID.
 CC PRINTS: PR00759; BASICPTASE.
 CC SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_EXTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT FT
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT CARBOHYD 289 289
 FT VARSPLIC 290 364
 FT SEQUENCE 770 AA; 86704 MW; C26C9DBB2D929A7 CRC64;

Query Match 100.0%; Score 11; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
 |||||||||
 DB 696 GSNKGATIGLM 706

RESULT 11
 PROF_ENTHI STANDARD: PRT: 130 AA.
 ID PROF_ENTHI
 AC P49230;
 DT 01-FEB-1996 (rel. 33, Created)
 DT 01-FEB-1996 (rel. 33, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE PROFILIN.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxId=5759;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 74-84 AND 86-94.
 RC STRAIN=SEL-3;
 RX MEDLINE=96085166; PubMed=8521867;
 RA Binder M., Orther S., Erben H., Scheiner O., Wiedermann G.,
 RA Valenta R., Duchene M.;
 RT "The basic isoform of profilin in pathogenic Entamoeba histolytica.
 RT cDNA cloning, heterologous expression, and actin-binding
 RT properties.";
 RL Eur. J. Biochem. 233:976-981(1995).
 CC -1- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE
 CC CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE
 CC POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW
 CC CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
 CC IP3 AND DG.
 CC -1- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC
 CC ACTIN IN A 1:1 RATIO.
 CC -1- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
 CC -----
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 CC EMBL; AB031291; BAA83499.1; -
 DR MGD; MG1:1926784; NP25.
 DR InterPro: IPR003247; CH_type.
 DR InterPro: IPR001715; Calponin_hom.
 DR InterPro: IPR000557; Calponin_repeat.
 DR InterPro: IPR003096; SM22_calponin.
 DR Pfam; PF0402; calponin; 1.
 DR Pfam; PF0307; CH; 1.
 DR PRINTS; PR00888; SM22CALPONIN.
 DR PRINTS; PR00890; TRANGELIN.
 DR PRODOM; PD001527; CH_type; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS01052; CALPONIN; 1.
 DR PROSITE; PS50021; CH; 1.
 DR DOMAIN 24 136 CH.
 FT REPEAT 174 199 CALPONIN-LIKE 26 AA MOTIF.
 SQ SEQUENCE 199 AA; 22471 MW; 53802F6F94958202 CRC64;

Query Match 54.5%; Score 6; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGA 6
 DB 179 GSNKGA 184

RESULT 14
 NP25_RAT
 ID NP25_RAT STANDARD; PRT; 219 AA.
 AC P37805; Q09025;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NEURONAL PROTEIN NP25.
 GN NP25.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94285742; PubMed=8015377;
 RA Ren W.-Z., Ng G.Y.K., Wang R.-X., Wu P.H., O'Dowd B.F., Osmond D.H.,
 RA George S.R., Lew C.-C.;
 RT "The identification of NP25: a novel protein that is differentially
 RT expressed by neuronal subpopulations.";
 RL Brain Res. Mol. Brain Res. 22:173-185(1994).
 CC -1- TISSUE SPECIFICITY: ABUNDANT AND UBICUITOUS EXPRESSION IN NEURONS.
 CC -1- SIMILARITY: BELONGS TO THE CALPONIN FAMILY.

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 CC EMBL; M84725; AAC42095.1; -
 DR InterPro: IPR003247; CH_type.
 DR InterPro: IPR001715; Calponin_hom.
 DR InterPro: IPR000557; Calponin_repeat.
 DR InterPro: IPR003096; SM22_calponin.
 DR Pfam; PF0402; calponin; 1.

DR Pfam; PF0307; CH; 1.
 DR PRINTS; PR00888; SM22CALPONIN.
 DR PRINTS; PR00890; TRANGELIN.
 DR PRODOM; PD001527; CH_type; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS01052; CALPONIN; 1.
 DR PROSITE; PS50021; CH; 1.
 DR DOMAIN 24 136 CH.
 FT REPEAT 174 199 CALPONIN-LIKE 26 AA MOTIF.
 SQ SEQUENCE 219 AA; 24712 MW; 7A743BA6851DDDC7 CRC64;

Query Match 54.5%; Score 6; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGA 6
 DB 179 GSNKGA 184

RESULT 15
 FLAG_RHIME
 ID FLAG_RHIME STANDARD; PRT; 262 AA.
 AC O52946;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FLAGELLAR BASAL-BODY ROD PROTEIN FLAG (DISTAL ROD PROTEIN).
 GN FLAG.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RUI1/001;
 RA Platzer J., Schmitt R.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
 CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
 CC MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS OF
 CC FLAG IN THE DISTAL PORTION, AND FLAG, FLAG AND FLAG ARE THOUGHT TO
 CC BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS
 CC EACH (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
 CC FAMILY.

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 CC EMBL; L49337; AAB0413.1; -
 DR InterPro: IPR001444; Flag_bb_rod.
 DR Pfam; PF00460; Flag_bb_rod; 1.
 DR PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
 KW Flagella.
 SQ SEQUENCE 262 AA; 28062 MW; 738B0B953BAE293C CRC64;

Query Match 54.5%; Score 6; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GATIGL 10
 DB 65 GATIGL 70

Wed Apr 24 09:48:05 2002

us-09-689-469-4.oli.rsp

Page 10

Search completed: April 24, 2002, 09:24:54
Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:36 ; Search time 66.28 Seconds
(without alignments)
12.293 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 54

Sequence: 1 GSNKGALIGLM 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	15	AA60369
2	54	100.0	11	16	AA60369
3	54	100.0	11	17	AA60369
4	54	100.0	11	18	AA60369
5	54	100.0	11	19	AA60369
6	54	100.0	11	19	AA60369
7	54	100.0	11	20	AA60369
8	54	100.0	11	21	AA60369
9	54	100.0	11	22	AA60369
10	54	100.0	11	22	AA60369
11	54	100.0	14	19	AA60369

12	54	100.0	14	22	AA60369	Amyloid beta-prote
13	54	100.0	14	22	AA60369	Amyloid beta-prote
14	54	100.0	14	22	AA60369	Amyloid beta-prote
15	54	100.0	14	22	AA60369	Amyloid beta-prote
16	54	100.0	24	22	AA60369	Amyloid beta-prote
17	54	100.0	24	22	AA60369	Amyloid beta-prote
18	54	100.0	26	20	AA60369	Human amyloidogeni
19	54	100.0	26	20	AA60369	Human amyloidogeni
20	54	100.0	26	20	AA60369	Human amyloidogeni
21	54	100.0	27	20	AA60369	Human amyloidogeni
22	54	100.0	32	22	AA60369	Partial sequence o
23	54	100.0	35	19	AA60369	Beta-amyloid pepti
24	54	100.0	35	20	AA60369	Beta-amyloid pepti
25	54	100.0	35	20	AA60369	Beta-amyloid pepti
26	54	100.0	35	20	AA60369	Beta-amyloid pepti
27	54	100.0	35	20	AA60369	Beta-amyloid pepti
28	54	100.0	35	22	AA60369	Beta-amyloid pepti
29	54	100.0	35	22	AA60369	Amyloid beta-prote
30	54	100.0	36	20	AA60369	Amyloid beta-prote
31	54	100.0	38	15	AA60369	Beta-amyloid (1-38
32	54	100.0	38	20	AA60369	Human tachykinin a
33	54	100.0	38	22	AA60369	Amyloid beta-prote
34	54	100.0	38	22	AA60369	Amyloid beta-prote
35	54	100.0	39	15	AA60369	Beta-amyloid (1-39
36	54	100.0	39	20	AA60369	Human amyloid beta
37	54	100.0	39	20	AA60369	Synthetic amyloid
38	54	100.0	39	21	AA60369	Human amyloid beta
39	54	100.0	40	14	AA60369	Human Receptor to
40	54	100.0	40	15	AA60369	Beta-amyloid pepti
41	54	100.0	40	18	AA60369	Beta-amyloid (1-40
42	54	100.0	40	18	AA60369	Amyloid beta prote
43	54	100.0	40	19	AA60369	Amyloid beta pepti
44	54	100.0	40	19	AA60369	Beta-amyloid pepti
45	54	100.0	40	22	AA60369	Human amyloid anti

ALIGNMENTS

RESULT 1
ID AAR60369 standard; peptide; 11 AA.
XX AAR60369;
AC AAR60369;
XX 15-MAR-1995 (first entry)
XX Beta-amyloid (25-35).
DE Beta-amyloid (25-35).
XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
OS Homo sapiens.
XX WO9417197-A.
XX 04-AUG-1994.
XX 24-JAN-1994; 94WO-JP00089.
XX 25-JAN-1993; 93JP-0010132.
XX 05-FEB-1993; 93JP-0019035.
XX 16-NOV-1993; 93JP-0286985.
XX 28-DEC-1993; 93JP-0334773.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Kitada C, Odaka A, Suzuki N;
XX WPI; 1994-264110/32.
XX Antibodies recognising specific parts of beta-amyloid - can be
PT used for diagnosis of diseases implicating beta-amyloid, such as

PT	Alzheimer's disease
XX	
PS	Claim 2; Page 84; 116pp: Japanese.
CC	
CC	Antibodies which recognise specific subfragments of the beta-amyloid
CC	protein are claimed. Specifically, the antibodies (which are pref.
CC	monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC	portion of beta-amyloid or they recognise residues 25-35 or 35-43
CC	from the C-terminal portion. The antibodies are useful for assaying
CC	beta-amyloid and its derivatives for diagnosis of Alzheimer's
CC	disease.
XX	
SQ	Sequence 11 AA;
OY	Query Match 100.0%; Score 54; DB 15; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00034; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 GSNKGAITGIM 11 Db 1 gsnkgai9lm 11
RESULT	2
AAR87948	
ID	AAR87948 standard; peptide: 11 AA.
AC	
AA	AAR87948:
DT	05-MAR-1996 (first entry)
DE	beta-amyloid (25-35) peptide.
KW	Alzheimer's disease; beta-amyloid; plaque; glycosaminoglycan;
RV	proteoglycan; A-beta.
OS	Synthetic.
PN	WO9506477-A1.
PD	09-MAR-1995.
PE	29-AUG-1994; 94WO-US09853.
PR	31-AUG-1993; 93US-0114942.
PA	(GLIA-) GLIATECH INC.
PI	-Brunden KR, Frederickson RCA, Gupta-Bansal R, Richtercook NJ;
DR	WP1; 1995-115259/15.
PT	Treating Alzheimer's disease by using cpds. that inhibit beta
PT	amyloid binding - to glycosaminoglycan(s)
XX	
PS	Claim 49; Page 64; 88pp: English.
CC	
CC	The invention relates to new chemical compounds which are peptides of
CC	formulae XXNX (I), XXNX2 (II) and X1NX2X3 (III), and peptides comprising
CC	the sequences (I), (II) or (III) and containing not greater than 8 amino
CC	acid residues. In the formulae, X is any amino acid with a cationic side
CC	chain, N and Z are neutral amino acids, and two of X1, X2 and X3 are
CC	amino acids with an anionic side chain and the third is an amino acid
CC	with an anionic or neutral side chain. Also new is the peptide
CC	Gly-Ser-Asn-Iys-gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is
CC	the latter undecapeptide which represents amino acids 25-35 of the
CC	beta-amyloid peptide A-beta.
CC	The peptides inhibit the binding of glycosaminoglycans and/or proteo-
CC	glycans to A-beta peptide and hence can be used for preventing the
CC	formation of amyloid plaques and for treating Alzheimer's disease.
XX	
SQ	Sequence 11 AA;

```

Query Match          100.0%: Score 54; DB 16; Length 11;
Best Local Similarity 100.0%: Pred. No. 0.00034;
Matches    11; Conservative   0; Mismatches   0; Indels     0; Gaps      0;

QY       1 GSNKGAIGLM 11
         |||
Db        1 gsnkgaiglm 11

RESULT      3
AAR92807
ID AAR92807 standard; peptide: 11 AA.
XX
AC AAR92807;
XX
DT 18-OCT-1996 (first entry)
XX
DE Human beta-amyloid 25-35.
XX
KW PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's disease;
KM Down's syndrome; inhibition; neurotoxicity; beta-amyloid 25-35.
XX
OS Homo sapiens.
XX
PN WO9607425-A1.
XX
PD 14-MAR-1996.
XX
PF 07-SEP-1995; 95WO-US10989.
XX
PR 09-SEP-1994; 94US-0306872.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Perlmutter DH;
XX
DR WPI: 1996-171392/17.
XX
PT Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor
PT - used for inhibiting amyloid-beta protein neurotoxicity in e.g.
PT Alzheimer's disease
XX
PS Claim 5; Page 18; 31pp; English.
XX
CC The peptides PB145, PB446 and PB96 can be used to inhibit the
CC neurotoxicity of the present peptide, beta-amyloid 25-35, and are
CC therefore useful in the treatment of Alzheimer's disease and Down's
CC syndrome.
XX
SC Sequence 11 AA;

Query Match          100.0%: Score 54; DB 17; Length 11;
Best Local Similarity 100.0%: Pred. NO. 0.00034;
Matches    11; Conservative   0; Mismatches   0; Indels     0; Gaps      0;

QY       1 GSNKGAIGLM 11
         |||
Db        1 gsnkgaiglm 11

RESULT      4
AAW23336
ID AAW23336 standard; peptide: 11 AA.
XX
AC AAW23336;
XX
DT 12-MAR-1998 (first entry)
XX
DE Amyloid beta peptide 2 used to inhibit damage to cells in Alzheimer's.
XX
```

XX Amyloid beta peptide; extracellular deposit; Alzheimer's disease;
KW neurite outgrowth; microglial activation; neuronal cell degeneration;
KM receptor for advanced glycosylation end product;
KW amyloid beta peptide fibril.
XX
OS Homo sapiens.
XX
PN WO9726913-A1.
XX
PD 31-JUL-1997.
XX
PF 21-JAN-1997; 97WO-US00857.
XX
PR 26-JAN-1996; 96US-0592070.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Schmidt AM, Stern D, Yan SD;
XX
DR WPI; 1997-393374/36.
XX
PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an
PT agent which inhibits interaction of an amyloid-beta peptide with a
PT receptor for advanced glycosylation end product
XX
PS Claim 5; Page 10; 91pp; English.
XX
CC Peptides AAM2335-36 are portions of the the amyloid beta peptide, which
CC is the principal component of extracellular deposits in Alzheimer's
CC disease. It has been shown to promote neurite outgrowth, generate
CC reactive oxygen intermediates, induce cellular oxidant stress, lead to
CC neuronal cytotoxicity, and promote microglial activation. The present
CC peptide, which comprises amino acids 25-35 of the amyloid beta peptide,
CC is used in a pharmaceutical composition. This composition comprises an
CC agent capable of inhibiting interaction of an amyloid-beta peptide with
CC a receptor for advanced glycosylation end product and a carrier. A
CC method for inhibiting interaction of amyloid beta peptide with a receptor
CC for advanced glycosylation on the surface of a cell comprises contacting
CC the cell with e.g. present peptide. Depending on the type of cell,
CC inhibiting the interaction between the amyloid beta peptide and the
CC receptor for advanced glycosylation can be used for inhibiting
CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta
CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid
CC beta peptide into a fibril, inhibiting aggregation of amyloid beta
CC peptide on the surface of a cell, inhibiting infiltration of a microglial
CC cell into senile plaques, and inhibiting activation of microglial cells
CC by amyloid beta peptide. The methods can be used for treating e.g.
CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic
CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia
CC associated with head trauma, amyotrophic lateral sclerosis, multiple
CC sclerosis or neuronal degeneration.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11
IIIIIIIIII
Db 1 gsnkgaiiglm 11

RESULT 5
AAM64497
ID AAM64497 standard; peptide; 11 AA.
XX
AC AAM64497;
XX
DT 20-OCT-1998 (first entry)
XX
DE Neurotoxic beta-amyloid peptide decoy peptide #10.

XX Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
KM aggregate; Alzheimers disease; decoy; treatment.
XX
OS Synthetic.
XX
PN WO9830229-A1.
XX
PD 16-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00653.
XX
PR 29-OCT-1997; 97US-0960188.
PR 10-JAN-1997; 97US-0035847.
XX
PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Blanchard BJ, Ingram VM;
XX
DR WPI; 1998-398795/34.
XX
PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by
PT administering decoy peptide or other calcium-influx inhibitor,
PT useful for, e.g. treating Alzheimer's disease
XX
PS Example 4; Page 42; 68pp; English.
XX
CC AAM64488-w64517 are decoy peptides that bind to a neurotoxic
CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
CC form aggregates that increase calcium influx into neuronal cells. Such
CC peptides can be used in the treatment of diseases associated with
CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
CC injection and orally, or from slow-release implants.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11
IIIIIIIIII
Db 1 gsnkgaiiglm 11

RESULT 6
AAM47231
ID AAM47231 standard; peptide; 11 AA.
XX
AC AAM47231;
XX
DT 22-MAY-1998 (first entry)
XX
DE Beta-amyloid peptide residues 25-35.
XX
KW Screening assay; beta-amyloid peptide; treatment;
KW amyloidosis disease; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5721106-A.
XX
PD 24-FEB-1998.
XX
PF 12-SEP-1994; 94US-0304585.
XX
PR 12-SEP-1994; 94US-0304585.
PR 13-AUG-1991; 91US-0744767.
XX
PA (HARD) HARVARD COLLEGE.
PA (MINN) UNIV MINNESOTA.

XX Maggio JE, Mantyh PW;
XX WPI; 1998-168404/15.
DR
XX
PT New in vitro screening assay for Alzheimer's disease drugs -
PT comprises assessing binding of labelled beta-amyloid peptide to silk
PT sample
XX
XX
PS Example 1; Columns 29-30; 36pp; English.
XX
CC The present sequence was used in the development of a novel in
CC vitro screening assay for agents capable of affecting the
CC deposition of beta-amyloid peptide (BAP) on tissue. The method
CC comprises contacting a silk sample with labelled BAP, optionally
CC in the presence of a test agent, detecting the amount of label
CC bound to the silk and assessing the effect of the agent on the
CC deposition of BAP. Agents that inhibit binding of BAP to silk are
CC potentially useful for treating amyloidosis diseases, especially
CC Alzheimer's disease.
CC
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
Db 1 gsnkgaliglm 11

RESULT 7
ID AAM81470 standard; peptide; 11 AA.
XX
AC AAM81470;
XX
DT 28-JAN-1999 (first entry)
XX
DE Synthetic amyloid beta (Abeta) peptide 5 (residues 25-35).
XX
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
OS Synthetic.
XX
PN US5840838-A.
XX
PD 24-NOV-1998.
XX
PF 29-FEB-1996; 96US-0609090.
XX
PR 29-FEB-1996; 96US-0609090.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
XX
DR WPI; 1999-034120/03.
XX
PT Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
XX
PS Claim 5; Columns 9-10; 14pp; English.
XX
CC Sequences AAM81466 to AAM81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/mL, incubating the

CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC "evaporative deposition," in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide-enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
CC
SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
Db 1 gsnkgaliglm 11

RESULT 8
ID AAY52133 standard; peptide; 11 AA.
XX
AC AAY52133;
XX
DT 28-JAN-2000 (first entry)
XX

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #2.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

PT Inhibiting tumour invasion of spreading by administration of soluble
PT receptor for advanced glycation endproducts -
XX
PS Claim 28; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble
CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
CC a range of physiologically and pathophysiologically relevant ligands
CC when considering tumour invasion. In normal developing neurons RAGE
CC colocalizes with amphoterin which is a matrix associated polypeptide.
CC The expression of both RAGE and amphoterin decreases after birth, but
CC both have increased expression in tumours. RAGE polypeptides
CC AAY52133-Y52135 are used in the invention in a method for inhibiting
CC tumour invasion and metastasis. The method involves inhibiting tumour
CC invasion and metastasis via administration of a therapeutically effective
CC amount of the pharmaceutical composition containing a RAGE polypeptide.
CC The invention also relates to a method for evaluating the ability of an
CC agent to inhibit tumour invasion in a local cellular environment. RAGE
CC can be administered to a patient in a pharmaceutically acceptable
CC carrier.

SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 111111111111
 Db 1 gsnkgaiiglm 11

RESULT 9

AAB91775
 ID AAB91775 standard; Peptide; 11 AA.

AC AAB91775;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:951.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 blood component; modification; succinimidyl; maleimido group; amino;
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT -

PS Disclosure; Page 504; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

CC Sequence 11 AA;

SQ

QY 1 GSNKGAIIGLM 11
 111111111111
 Db 1 gsnkgaiiglm 11

RESULT 10

AAB91808
 ID AAB91808 standard; Peptide; 11 AA.

AC AAB91808;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:984.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 blood component; modification; succinimidyl; maleimido group; amino;
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT -

PS Disclosure; Page 516; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

CC Sequence 11 AA;

SQ

Query Match 100.0%; Score 54; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
 111111111111
 Db 1 gsnkgaiiglm 11

RESULT 11

AAW64498 standard; peptide; 14 AA.

AAW64498:

20-OCT-1998 (first entry)

Neurotoxic beta-amyloid peptide decoy peptide #11.

Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx; aggregate; Alzheimers disease; decoy; treatment.

Synthetic.

WO9830229-A1.

16-JUL-1998.

09-JAN-1998; 98WO-US00653.

29-OCT-1997; 97US-0960188.

10-JAN-1997; 97US-0035847.

(MASI) MASSACHUSETTS INST TECHNOLOGY.

Blanchard BJ, Ingram VM;

WPI; 1998-398795/34.

Inhibition of aggregation of, e.g. beta-amyloid peptide - by administering decoy peptide or other calcium-influx inhibitor, useful for, e.g. treating Alzheimer's disease

Example 4; Page 43; 68pp; English.

AAW64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates that increase calcium influx into neuronal cells. Such peptides can be used in the treatment of diseases associated with neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and orally, or from slow-release implants.

Sequence 14 AA;

Query Match 100.0%; Score 54; DB 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00044; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 4 gsnkgatiglm 14

RESULT 12

AAB91782 standard; peptide; 14 AA.

AAB91782:

22-JUN-2001 (first entry)

Amyloid beta-protein fragment peptide SEQ ID NO:958.

Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidy1; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

Homo sapiens.

Synthetic.

WO200069900-A2.

23-NOV-2000.

17-MAY-2000; 2000WO-US13576.

17-MAY-1999; 99US-0134406.

10-SEP-1999; 99US-0153406.

15-OCT-1999; 99US-0159783.

(CONJ-) CONJUCHEM INC.

Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

WPI; 2001-112059/12.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

Disclosure; Page 507; 733pp; English.

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

Sequence 14 AA;

Query Match 100.0%; Score 54; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00044; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11

Db 4 gsnkgatiglm 14

RESULT 13

AAB91788 standard; peptide; 14 AA.

AAB91788:

22-JUN-2001 (first entry)

Amyloid beta-protein fragment peptide SEQ ID NO:964.

Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidy1; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

Homo sapiens.

Synthetic.

WO200069900-A2.

23-NOV-2000.

[illegible]

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PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
PA (CONU-) CONUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR WPI: 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
PS
PS Disclosure: Page 519; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (Iii) and a
CC reactive group (Iii) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (Iv), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 14 AA:
SQ
Query Match 100.0%; Score 54; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GSNKGAIGLM 11
|||||||
Db 4 gsnkgai19lm 14
RESULT 15
AAB91805
ID AAB91805 standard; Peptide: 24 AA.
AC AAB91805;
AC
AC
XX 22-JUN-2001 (first entry)
DT
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:981.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200069900-A2.
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONU-) CONUCHEM INC.
PA

```

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 PI
 XX
 DR MPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

PS Disclosure; Page 515; 733pp; English.

XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxy/thiol groups on blood components to form a
 CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 54; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred No. 0.00078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGALIGLM 11
 |||||
 Db 9 gsnkgaliglm 19

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 Job time: 140 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:15 ; Search time 32.34 Seconds
(without alignments)
7.654 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 54
Sequence: 1 GSNKGATIGLM 11

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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	1	US-07-744-767A-3 Sequence 3, Appl1
2	54	100.0	11	1	US-08-306-872-2 Sequence 2, Appl1
3	54	100.0	11	1	US-08-346-849-5 Sequence 5, Appl1
4	54	100.0	11	1	US-08-304-585-3 Sequence 3, Appl1
5	54	100.0	11	1	US-08-302-808-8 Sequence 8, Appl1
6	54	100.0	11	2	US-08-433-734-3 Sequence 3, Appl1
7	54	100.0	11	2	US-08-609-090-5 Sequence 5, Appl1
8	54	100.0	11	2	US-08-986-948-8 Sequence 8, Appl1
9	54	100.0	11	2	US-08-293-284A-5 Sequence 5, Appl1
10	54	100.0	11	4	US-09-005-215-10 Sequence 10, Appl1
11	54	100.0	11	5	PCT-US95-10989-2 Sequence 2, Appl1
12	54	100.0	14	4	US-09-005-215-11 Sequence 11, Appl1
13	54	100.0	26	1	US-08-304-585-7 Sequence 7, Appl1
14	54	100.0	34	2	US-08-475-579A-4 Sequence 4, Appl1
15	54	100.0	35	1	US-08-304-585-6 Sequence 6, Appl1
16	54	100.0	35	2	US-08-612-785B-16 Sequence 16, Appl1
17	54	100.0	35	2	US-08-612-785B-36 Sequence 36, Appl1
18	54	100.0	35	2	US-08-612-785B-39 Sequence 39, Appl1
19	54	100.0	36	2	US-08-609-090-6 Sequence 6, Appl1
20	54	100.0	38	2	US-08-302-808-1 Sequence 1, Appl1
21	54	100.0	38	2	US-07-737-371E-68 Sequence 68, Appl1
22	54	100.0	38	2	US-08-986-948-1 Sequence 1, Appl1
23	54	100.0	39	1	US-08-304-585-5 Sequence 5, Appl1
24	54	100.0	39	1	US-08-302-808-2 Sequence 2, Appl1
25	54	100.0	39	2	US-08-609-090-7 Sequence 7, Appl1
26	54	100.0	39	2	US-08-682-245A-1 Sequence 1, Appl1
27	54	100.0	39	2	US-08-682-245A-1 Sequence 1, Appl1

28	54	100.0	39	2	US-08-986-948-2 Sequence 2, Appl1
29	54	100.0	40	1	US-07-744-767A-1 Sequence 1, Appl1
30	54	100.0	40	1	US-08-235-400-2 Sequence 2, Appl1
31	54	100.0	40	1	US-08-476-464A-2 Sequence 2, Appl1
32	54	100.0	40	1	US-08-304-585-1 Sequence 1, Appl1
33	54	100.0	40	1	US-08-304-585-8 Sequence 8, Appl1
34	54	100.0	40	1	US-08-302-808-3 Sequence 3, Appl1
35	54	100.0	40	2	US-08-433-734-1 Sequence 1, Appl1
36	54	100.0	40	2	US-08-609-090-8 Sequence 8, Appl1
37	54	100.0	40	2	US-07-737-371E-69 Sequence 69, Appl1
38	54	100.0	40	2	US-08-682-245A-2 Sequence 2, Appl1
39	54	100.0	40	2	US-08-986-948-3 Sequence 3, Appl1
40	54	100.0	40	2	US-08-461-216-1 Sequence 1, Appl1
41	54	100.0	40	4	US-08-959-148-1 Sequence 1, Appl1
42	54	100.0	40	5	PCT-US92-06700-1 Sequence 1, Appl1
43	54	100.0	41	1	US-07-819-361-1 Sequence 1, Appl1
44	54	100.0	41	1	US-08-302-808-4 Sequence 4, Appl1
45	54	100.0	41	2	US-08-682-245A-3 Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-07-744-767A-3
; Sequence 3, Application US/07744767A
; Patent No. 5434050
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled - Amyloid Peptide and Methods
; TITLE OF INVENTION: for use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07744, 767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muelling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-744-767A-3

Query Match 100.0%; Score 54; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
|||||
Db 1 GSNKGATIGLM 11

RESULT 2
US-08-306-872-2
Sequence 2, Application US/08306872
Patent No. 5514653
GENERAL INFORMATION:
APPLICANT: Perlmutter, David H.
TITLE OF INVENTION: Method of Blocking the SEC Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,872
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-2833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-306-872-2

Query Match 100.0%; Score 54; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
Db 1 GSNKGATIGLM 11

RESULT 3
US-08-346-849-5
Sequence 5, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-5

Query Match 100.0%; Score 54; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
Db 1 GSNKGATIGLM 11

RESULT 4
US-08-304-585-3
Sequence 3, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantlyn, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 361415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
US-08-304-585-3

Query Match 100.0%; Score 54; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|1111111111|
DB 1 GSNKGAIIGLM 11

RESULT 5

US-08-302-808-8
; Sequence 8, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhlro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3440
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-8

Query Match 100.0%; Score 54; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|1111111111|
DB 1 GSNKGAIIGLM 11

RESULT 6

US-08-433-734-3
; Sequence 3, Application US/08433734
; Patent No. 5837473
; GENERAL INFORMATION:
; APPLICANT: Magglio, John E.
; APPLICANT: Mantyh, Patrick W. -Amyloid Peptide and Methods
; TITLE OF INVENTION: Labelled
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muelting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-734-3

Query Match 100.0%; Score 54; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|1111111111|
DB 1 GSNKGAIIGLM 11

RESULT 7
US-08-609-090-5
; Sequence 5, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: ARSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-5

Query Match 100.0%; Score 54; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
|||||
DB 1 GSNKGATIGLM 11

RESULT 8
US-08-986-948-8
Sequence 8, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uharo
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-8

Query Match 100.0%; Score 54; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
|||||
DB 1 GSNKGATIGLM 11

RESULT 9
US-08-293-284A-5
Sequence 5, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuangang
APPLICANT: Rich, Alexander
APPLICANT: Dipersio, C. Michael
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:


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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/005,215
8  FILING DATE:
9  CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: 08/960,188
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0656/7035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-2441
TELEFAX: 617-720-3500
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-09-005-215-11

Query Match 100.0%; Score 54; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 4 GSNKGATIGLM 14

RESULT 13
US-08-304-585-7
Sequence 7, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglo, John E.
ATTORNEY/AGENT INFORMATION:
NAME: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-304-585-7

Query Match 100.0%; Score 54; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 16 GSNKGATIGLM 26

RESULT 14
US-08-475-579A-4
Sequence 4, Application US/08475579A
Patent No. 5854215
GENERAL INFORMATION:
APPLICANT: Mark A. Findeis et al.
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "symbol")-Amyloid Peptide Aggre
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,579A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: PPI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-475-579A-4

Query Match 100.0%; Score 54; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 19 GSNKGATIGLM 29

RESULT 15
US-08-304-585-6
Sequence 6, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglo, John E.
ATTORNEY/AGENT INFORMATION:
NAME: Mantyh, Patrick W.

;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.
;; STREET: P.O. Box 581415
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55458-1415
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/304,585
;; FILING DATE: 12-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mueling, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 110.00010120
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-305-1217
;; TELEFAX: 612-305-1228
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; US-08-304-585-6

Query Match 100.0%; Score 54; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSNKGAIIGLM 11
|||||
DB 25 GSNKGAIIGLM 35

Search completed: April 24, 2002, 09:18:15
Job time: 174 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:25 ; Search time 63.44 Seconds
(without alignments)
25.362 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 11
Sequence: 1 GSNKGATIGLM 11

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.virus:*
14: sp.vertebrate:*
14: sp.unclassified:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	11	100.0	79	11	035463 cricetus
3	11	100.0	82	4	P78438
4	11	100.0	82	4	Q16014
5	11	100.0	82	4	Q16019
6	11	100.0	82	4	Q16020
7	11	100.0	97	4	Q13778
8	11	100.0	534	13	093296
9	11	100.0	569	13	093296
10	11	100.0	607	11	098K32
11	11	100.0	693	11	098K32
12	11	100.0	693	11	098SG0
13	11	100.0	695	11	P97487
14	11	100.0	695	11	Q60436
15	11	100.0	695	13	09DGJ8
16	11	100.0	695	13	098SF9
17	11	100.0	699	13	057394
18	11	100.0	737	13	093279
19	11	100.0	747	13	Q91963
					Q9DGJ7

20	11	100.0	770	6	09TU10	09tu10 sus scrofa
21	11	100.0	780	13	073683	073683 tetraodon f
22	10	90.9	612	13	0919E7	0919e7 brachydanio
23	9	81.8	33	4	09UC37	09uc33 homo sapien
24	7	63.6	247	2	09KBT2	09kbt2 bacillus ha
25	7	63.6	828	10	09FGRL	09fgrl arabidopsis
26	6	54.5	20	4	09UCB6	09ucb6 homo sapien
27	6	54.5	30	4	09UCA9	09uca9 homo sapien
28	6	54.5	130	6	029364	029364 sus scrofa
29	6	54.5	131	5	024897	024897 echinococu
30	6	54.5	143	11	09D6K2	09d6k2 mus musculu
31	6	54.5	144	2	09AM08	09am08 plectonema
32	6	54.5	157	10	09C5F3	09c5f3 arabidopsis
33	6	54.5	175	5	09VZ11	09vz11 drosophila
34	6	54.5	176	2	09KCS1	09kcs1 bacillus ha
35	6	54.5	188	5	09NHZ2	09nhz2 drosophila
36	6	54.5	190	5	024799	024799 echinococu
37	6	54.5	192	5	093713	093713 caenorhabd
38	6	54.5	192	5	09U4H8	09u4h8 caenorhabd
39	6	54.5	205	2	09WXS1	09wxs1 thermotoga
40	6	54.5	205	2	09KXK7	09kxk7 vibrio chol
41	6	54.5	216	11	09JMA4	09jma4 mus musculu
42	6	54.5	216	11	09JMA26	09jma26 mus musculu
43	6	54.5	223	11	09Z1U9	09z1u9 mus musculu
44	6	54.5	230	2	09KMA3	09kma3 vibrio chol
45	6	54.5	234	2	007221	007221 mycobacteri

ALIGNMENTS

RESULT 1
ID 097917 PRELIMINARY; PRT; 49 AA.
AC 097917;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
GN AFP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Re-sequencing of DNA from a diverse panel of cattle reveals frequent
RT polymorphisms in both intron and exon."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A013033; CAB38017.1; -
DR HSSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 100.0%; Score 11; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
DB 8 GSNKGATIGLM 18

RESULT 2
ID 035463 PRELIMINARY; PRT; 79 AA.
AC 035463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).
 GN BETA APP.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB6608.1; -;
 DR HSSP; P05067; 1QCM.
 FT NON_TER 1 79 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 8538 MW; 37E2C6C3BFF3E597 CRC64;

Query Match 100.0%; Score 11; DB 11; Length 79;
 Best Local Similarity 100.0%; Pred. No. 5, 6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
 DB 45 GSNKGATIGLM 55

RESULT 3
 ID P78438 PRELIMINARY; PRT; 82 AA.
 AC P78438;
 DT 01-MAY-1997 (TREMURel. 03, Created)
 DT 01-MAY-1997 (TREMURel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
 GN APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89392030; PubMed=2675837;
 RA Johnston E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [2]
 RP SEQUENCE OF 19-48 FROM N.A.
 RX MEDLINE=87120329; PubMed=2949367;
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
 RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic
 RT linkage near the Alzheimer locus."
 RL Science 235:880-884(1987).
 RN [3]
 RP SEQUENCE OF 32-63 FROM N.A.
 RX MEDLINE=9305397; PubMed=1415269;
 RA Kamino K., Orr H.T., Payami H., Wiseman E.M., Alonso M.E., Pulst S.M.,
 RA Anderson L., O'dahl S., Nemens E., White J.A.;
 RT "Linkage and mutational analysis of familial Alzheimer disease
 RT kinds for the APP gene region."
 RL Am. J. Hum. Genet. 51:998-1014(1992).
 DR EMBL; M28270; AAA51768.1; -;
 DR EMBL; M29269; AAA51768.1; JOINED.
 DR EMBL; M15532; AAA51564.1; -;
 DR EMBL; S45136; AAB23646.1; -;
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 82 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
 DB 41 GSNKGATIGLM 51

RESULT 4
 ID Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S60721; AAB26263.2; -;
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 82 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
 DB 42 GSNKGATIGLM 52

RESULT 5
 ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61380; AAB26264.2; -;
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 82 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
DB 42 GSNKGATIGLM 52

RESULT 6

ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93236601; PubMed-8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB2625.2; -.
DR HSSP; P05067; 1BA4. 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
DB 42 GSNKGATIGLM 52

RESULT 7

ID Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-87120328; PubMed-3810169;
RA Goldgaber D., Ierman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDBA48DE474E CRC64;

Query Match 100.0%; Score 11; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
DB 23 GSNKGATIGLM 33

RESULT 8

ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RN [1]
RP SEQUENCE FROM N.A.
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a substrate for Caspase 3 in dying motoneurons."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
DB 460 GSNKGATIGLM 470

RESULT 9

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 100.0%; Score 11; DB 13; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 496 GSNKGATIGLM 506

RESULT 10
 ID 099K32 PRELIMINARY; PRT; 607 AA.
 AC 099K32;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR;
 RA Stralsberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005490; AAH05490.1; -
 FT NON_TER 1
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 100.0%; Score 11; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 533 GSNKGATIGLM 543

RESULT 11
 ID 098SG0 PRELIMINARY; PRT; 693 AA.
 AC 098SG0;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE BETA-AMYLLOID PRECURSOR PROTEIN A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 DR University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -
 KW SIGNAL.
 FT SIGNAL 1
 SQ SEQUENCE 693 AA; 78568 MW; CAFID655C1AB53 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 693;
 Best Local Similarity 100.0%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSNKGATIGLM 11
 DB 619 GSNKGATIGLM 629

RESULT 12
 ID P97487 PRELIMINARY; PRT; 695 AA.
 AC P97487; P97942;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE HIPPOCAMPAL AMYLOID PROTEIN.
 GN APP.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN 12

RP SEQUENCE OF 581-662 FROM N.A.
 RC STRAIN=129SV;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capechi M.,
 RA Loring J.F., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U84012; AAB41502.1; -
 DR EMBL; U82624; AAB40919.1; -
 DR HSSP; P05067; 1OCM.
 DR MGD; MGI:88059; App.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; Pf02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 100.0%; Score 11; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 621 GSNKGATIGLM 631

RESULT 13
 ID 060496 PRELIMINARY; PRT; 695 AA.
 AC 060496;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Beck M., Mueller D., Bigl V.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
 DR EMBL: X97631; CAA66230.1; -.
 DR HSSP: P05067; IBA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 11; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 621 GSNKGATIGLM 631

RESULT 14

Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE BETA-AMYL0ID PRECURSOR PROTEIN 695 ISOFORM.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289218; AAG00593.1; -.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 621 GSNKGATIGLM 631

RESULT 15

Q98SF9 PRELIMINARY; PRT; 695 AA.
 AC Q98SF9;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE BETA-AMYL0ID PRECURSOR PROTEIN B.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 DR University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ298151; CAC37194.1; -.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 100.0%; Score 11; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 DB 621 GSNKGATIGLM 631

Search completed: April 24, 2002, 09:24:25
 Job time: 249 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: April 24, 2002, 09:19:00 ; Search time 38.71 Seconds
(without alignments)
21.646 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 54
Sequence: 1 GSNKGATIGLM 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	42	2	PN0512
2	54	100.0	57	2	E60045
3	54	100.0	57	2	F60045
4	54	100.0	57	2	G60045
5	54	100.0	57	2	D60045
6	54	100.0	57	2	A60045
7	54	100.0	57	2	B60045
8	54	100.0	82	2	P00438
9	54	100.0	695	1	A43795
10	54	100.0	695	1	A27485
11	54	100.0	695	2	S00550
12	54	100.0	747	2	JH0773
13	54	100.0	770	1	ORHUA4
14	41	75.9	247	2	B83880
15	38	70.4	229	2	C69971
16	38	70.4	300	2	S47764
17	38	70.4	300	2	B86028
18	37	68.5	216	2	T29039
19	37	68.5	906	2	A43817
20	36	66.7	305	2	S75667
21	36	66.7	390	1	TVMVCB
22	36	66.7	417	2	F70681
23	36	66.7	496	2	JC5170
24	36	66.7	661	1	A42287
25	36	66.7	896	2	A43817
26	35	64.8	238	2	E70337
27	35	64.8	309	2	G75286
28	35	64.8	309	2	A44121
29	35	64.8	414	1	I38977

30	35	64.8	486	2	B70504	probable transmem
31	35	64.8	593	2	A96783	unknown protein r2
32	35	64.8	673	2	B70528	probable peptidase
33	35	64.8	699	2	A96529	hypothetical prote
34	34	63.0	269	2	S65034	cytochrome-c oxida
35	34	63.0	308	2	S67657	hypothetical prote
36	36	63.0	315	2	S76043	hypothetical prote
37	34	63.0	323	2	S25513	outer membrane pro
38	34	63.0	345	2	E64458	branched-chain am
39	34	63.0	503	2	S73843	general amino acid
40	34	63.0	605	2	S67815	protein-tyrosine k
41	34	63.0	660	2	B70662	probable membrane
42	41	63.0	1362	2	T41534	leptomycin B resis
43	33	61.1	161	2	H71677	invasion protein A
44	33	61.1	169	2	B83640	hypothetical prote
45	33	61.1	293	2	J00380	proteinase T (EC 3

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A:Reference number: PN0512; MID:9320653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SH1>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 54; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
DB 25 GSNKGATIGLM 35

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
DB 30 GSNKGATIGLM 40

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 54; DB 2; Length 57;
 Best local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 30 GSNKGATIGLM 40

RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 54; DB 2; Length 57;
 Best local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 30 GSNKGATIGLM 40

RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 54; DB 2; Length 57;
 Best local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 30 GSNKGATIGLM 40

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; PMID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 54; DB 2; Length 57;
 Best local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 30 GSNKGATIGLM 40

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; PMID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

100.0%; Score 54; DB 2; Length 57;
 Best local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 30 GSNKGATIGLM 40

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; PMID:93075180

A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DNA>
A:Cross-references: GB:M83558; GB:M83657
R:Jomuncione, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <DNA>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 54; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|||||
DB 41 GSNKGAIIGLM 51

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|||||
DB 621 GSNKGAIIGLM 631

RESULT 10
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A:Reference number: A27485; MUID:88106489
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458

A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Rizumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
A:Reference number: I49485; MUID:92209998
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RBS>
A:Cross-references: GB:DJ0603; NID:q220328; PIDN:BAA01456.1; PID:q220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 54; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
|||||
DB 621 GSNKGAIIGLM 631

RESULT 11
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
A:Reference number: S00550; MUID:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; PID:q55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saltch, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37 'X', 39-40 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, U.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 54; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 621 GSNKGAIIGLM 631

RESULT 12

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: Larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 54; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
DB 673 GSNKGAIIGLM 683

RESULT 13

ORH04
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A34466; I39452; I39453; I59562; A44
4688; A28583; A29302; A60803; JH0038; S06121; A60353; A59011; A38384; S29076; S38252; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PRA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:Jia Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
R:Toshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:q178616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530, 'QMLMPVIAPEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615
R:Toshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Accession: I39453
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anders
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93055397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIRP:115574)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LT
A:Note: sequence extracted from NCBI backbone (NCBIRP:115576)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
Nature 325, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526
 A>Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M6765; NID:9178539; PIDN:AA51722.1; PID:9178540
 A>Note: the authors translated the codon CAG for residue 647 as Asp
 R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M5533; NID:9178706; PIDN:AA35540.1; PID:9178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANL>
 A:Cross-references: GB:M5532; NID:9177957; PIDN:AA51564.1; PID:9177958
 R:Dykes, T.; Weidmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lampetti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9293612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A>Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
 Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721
 A>Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9293611
 A:Experimental source: glioblastoma cell line
 A>Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320

A:Accession: A30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AA51726.1; PID:9178573
 A>Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTC for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A>Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GSNKGAITGL 11
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 Db 696 GSNKGAITGL 706
 RESULT 14
 B83880
 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [Imported] - Bacillus halodurans (s
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence-revision 01-Dec-2000 #text-change 31-Dec-2000
 C:Accession: B83880
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20263314
 A:Accession: B83880
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-247 <STO>
 A:Cross-references: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA805561.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH1842
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 Query Match 75.9%; Score 41; DB 2; Length 247;
 Best Local Similarity 80.0%; Pred. No. 3.2;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GSNKGAITGL 10
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 Db 156 GASKGATIGL 165
 RESULT 15
 C69971
 conserved hypothetical protein yrak - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 15-Oct-1999
 C:Accession: C69971
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod, akuchl, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; M0ID:98044033
 A:Accession: C69971
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-229 <RUN>
 A:Cross-References: GB:299117; GB:AL009126; NID:g2634966; PIDN:CAB14632.1; PID:e183920;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yrak

Query Match 70.4%; Score 38; DB 2; Length 229;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSMKGATIGL 10
 11:11:1111
 DB 97 GSSSGAVIGL 106

Search completed: April 24, 2002, 09:19:01
 Job time: 200 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:38 ; Search time 21.42 Seconds

(without alignments)
18.829 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 54

Sequence: 1 GSNKGATIGLM 11

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	54	100.0	57	A4_PIG	Q29023 sus scrofa
2	54	100.0	57	A4_URSWA	Q29149 ursus marit
3	54	100.0	58	A4_CANFA	Q28280 canis fami
4	54	100.0	58	A4_RABIT	Q28748 oryctolagus
5	54	100.0	58	A4_SHEEP	Q28757 ovis aries
6	54	100.0	59	A4_BOVIN	Q28053 bos taurus
7	54	100.0	751	A4_SAISC	Q95241 salmtr1 sc
8	54	100.0	770	A4_HUMAN	P05067 homo sapien
9	54	100.0	770	A4_MOUSE	P12023 mus musculu
10	54	100.0	770	A4_RAT	P08592 rattus norv
11	38	70.4	300	DPPC_ECOLI	P37315 escherichia
12	37	68.5	906	CB1_HUMAN	P22681 homo sapien
13	36	66.7	305	RS1B_STNY3	P74142 synchocyst
14	36	66.7	390	CB1_MLVN	P23092 cas-n-1 mu
15	36	66.7	496	MGLA_TREPA	Q56342 treponema p
16	36	66.7	661	RDGC_DROME	P40421 drosophila
17	36	66.7	896	CB1_MOUSE	P22682 mus musculu
18	35	64.8	146	Y237_AQDAE	O66425 aquifex aeo
19	35	64.8	295	DPPC_HAEIN	P51000 haemophilus
20	35	64.8	411	RR1_SPTOL	P23044 spinacia ol
21	34	63.0	269	COX3_TIRIU	Q36837 trichophyto
22	34	63.0	315	ERA_SYNY3	O55526 synchocyst
23	34	63.0	503	Y226_MYCPN	P75462 mycoplasma
24	34	63.0	605	RTK2_GEOCY	P42159 geodia cydo
25	34	63.0	1362	PMO1_SCHPO	P36619 schizosacch
26	33	61.1	161	NMDH_RICPR	O92619 rickettsia
27	33	61.1	293	PRTT_TRIAL	P20015 bacillus su
28	33	61.1	368	GRBB_BACSU	P39570 bacillus su
29	33	61.1	407	VG02_HSV1	O00126 icetaurid h
30	33	61.1	543	SGUT_VIBPA	P96169 vibrio para
31	33	61.1	649	PTMA_VIBCH	Q9KRG7 vibrio chol
32	33	61.1	653	PPH1_HUMAN	O14829 homo sapien
33	33	61.1	687	HS7E_DROME	P29845 drosophila

34	33	61.1	700	1	NONA_DROME	Q04047 drosophila
35	33	61.1	917	1	SLAP_THETH	P35830 thymus aqu
36	33	61.1	1648	1	RPO_CGMVS	P19523 cucumis gr
37	32	59.3	139	1	Y965_MYCTU	P71545 mycobacteri
38	32	59.3	360	1	Y463_MYCTU	O53411 mycobacteri
39	32	59.3	473	1	DLDH_BUCAT	P57303 buchnera ap
40	32	59.3	496	1	IA12_ARATH	O06402 arabidopsis
41	32	59.3	547	1	Y0T5_CAEEL	O09316 caenorhabdi
42	32	59.3	576	1	Y006_CAEEL	P34644 caenorhabdi
43	32	59.3	589	1	CAH_DUNSA	P54212 dunaliella
44	32	59.3	595	1	CR11_NEUCR	P21334 neuropept
45	32	59.3	753	1	PPH2_HUMAN	O14830 homo sapien

ALIGNMENTS

RESULT	ID	STANDARD:	PRT:	57 AA.
AC	A4_PIG	Q29023;		
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).			
DE	APP.			
GN	Sus scrofa (Pig).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_Taxid=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=92017079; PubMed=1656157;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis";			
RT	Brain Res. Mol. Brain Res. 10:289-305(1991).			
RL	Brain Res. Mol. Brain Res. 10:289-305(1991).			
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: X56127; CAA39592.1; -			
DR	HSP: P05067; IAML.			
DR	InterPro: IPR001868; A4_APP.			
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.			
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.			
FW	Glycoprotein; Amyloid; Neurone; Transmembrane.			
FT	NON_TER	1		
FT	CHAIN	1	48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	<1	33	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	34	57	POTENTIAL.
FT	NON_TER	57		
SO	SEQUENCE	57 AA; 6172 MW; 84209D88EBA82DFA CRC64;		

Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 GSNKGATIGLM 40

RESULT 2

AC_URSMA STANDARD: PRT: 57 AA.

ID A4_URSMA

AC 029149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Ursus maritimus (Polar bear) (Thalassos maritimus).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

CC G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X56128; CAA39593.1; -.

DR HSSP; P05067; IAML.

DR InterPro; IPR001868; A4_APP.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT NON_TER

FT SEQUENCE

57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match

Best Local Similarity 100.0%; Score 54; DB 1; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 GSNKGATIGLM 40

Y 1 GSNKGATIGLM 11

IIIIIIIIII

AC 028280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

CC G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

DR EMBL; X56125; CAA39590.1; -.

DR HSSP; P05067; IAML.

DR InterPro; IPR001868; A4_APP.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT NON_TER

FT SEQUENCE

58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match

Best Local Similarity 100.0%; Score 54; DB 1; Length 58;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 GSNKGATIGLM 41

Y 1 GSNKGATIGLM 11

IIIIIIIIII

AC 028748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
   |||
Db 30 GSNKGAIIGLM 40

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
RT INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
RT G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

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CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
   |||
Db 30 GSNKGAIIGLM 40

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
RT INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
RT G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

FT NON_TER 1 1
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 58 POTENTIAL.
 FT DOMAIN 57 >59 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 59 59
 SO SEQUENCE 59 AA; 6414 MW; F43469D48BA2E12D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 31 GSNKGATIGLM 41

RESULT 7
 A4_SAIISC STANDARD; PRT; 751 AA.

ID A4_SAIISC
 AC 095241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 DR EMBL: S81024; AAD14347.1;
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PRO0203; AMYLOIDA4.
 DR PRINTS: PRO0204; BETAAMYLOID.
 DR PRINTS: PRO0759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KJ; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRN; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KM Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT DOMAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC...) (PROBABLE).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC...) (PROBABLE).
 SO SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
 |||||
 Db 677 GSNKGATIGLM 687

RESULT 8
 A4_HUMAN STANDARD; PRT; 770 AA.

ID A4_HUMAN
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
 GN APP OR A4 OR CVAP OR AD1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor."
 RL Nature 325:733-736(1987).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=88122639; PubMed=2893289;
 CC Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hau D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors."
 RL Nature 331:525-527(1988).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=89128427; PubMed=2783775;
 CC Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons."
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97263807; PubMed=9108164;
 RX Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,

RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RA MEDLINE-8812640; PubMed-2893290;
 RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RA MEDLINE-8812641; PubMed-2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RA MEDLINE-87231971; PubMed-3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RA MEDLINE-88124954; PubMed-2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RA MEDLINE-88035004; PubMed-3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tountoulotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiotensin of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RA MEDLINE-90236318; PubMed-2110105;
 RA Yoshikata S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RA TISSUE-LIVER;
 RC MEDLINE-89016647; PubMed-3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RA MEDLINE-87250462; PubMed-3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RA MEDLINE-89384866; PubMed-2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Slinn S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RA MEDLINE-90211252; PubMed-19669731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RA MEDLINE-93188965; PubMed-8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RA MEDLINE-99215582; PubMed-10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RA MEDLINE-91104913; PubMed-2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RA MEDLINE-92031488; PubMed-1718421;
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamarch M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RA MEDLINE-94281210; PubMed-7516706;
 RA Talaoui J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RA MEDLINE-97128622; PubMed-8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RA MEDLINE-98359783; PubMed-9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RA MEDLINE-20400066; PubMed-10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RA MEDLINE-88296437; PubMed-2900137;

RA Dykx T., Weidemann A., Multaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RL EMBL J. 7:949-957(1988).
 RN [24]
 RP REVIEW.
 RX MEDLINE=92271194; PubMed=1589757;
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective.";
 RL Science 256:780-783(1992).
 RN [25]

Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAITGLM 11
 DB 696 GSNKGAITGLM 706

RESULT 9
 A4_MOUSE STANDARD; PRT; 770 AA.
 ID A4_MOUSE
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Bergh H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL gene 112:189-195(1992).
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Donura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC -----
 CC EMBL: X59379; -; NOT ANNOTATED_CDS.
 CC EMBL: M18373; AAA37139.1; -;
 CC EMBL: X15210; CAA33280.1; -;
 CC EMBL: D10603; BAA01436.1; -;
 CC EMBL: M24397; AAA39929.1; -;
 CC PIR: A27485; A27485.
 CC PIR: S04855; S04855.
 CC PIR: S19727; S19727.
 CC MGD: MGI:88059; APP.
 CC InterPro: IPR001868; A4-APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4-EXTRA; 1.
 CC Pfam: PF00144; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRINTS: PR00204; BETAAMYLOID.
 CC PRINTS: PR00759; BASICPTASE.
 CC SMART: SM00006; A4-EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4-EXTRA; 1.
 CC PROSITE: PS00320; A4-INTRA; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 CC PROSITE: PS50279; Amyloid; Neurone; Transmembrane; Signal;
 CC KW Alternative splicing; Serine protease inhibitor.
 CC FT SIGNAL 1 17
 CC CHAIN 18 770
 CC FT
 CC DOMAIN 18 699
 CC TRANSMEM 700 723
 CC DOMAIN 724 770
 CC DOMAIN 673 715
 CC DOMAIN 287 345
 CC SITE 759 762
 CC SITE 291 341
 CC DISULFID 291 341
 CC DISULFID 316 337
 CC CARBOHYD 542 542
 CC CARBOHYD 571 571
 CC CARBOHYD 289 289
 CC VARSPLIC 290 364
 CC VARSPLIC 346 380
 CC SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;

Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIIGLM 11
 |||||
 DB 696 GSNKGAIIIGLM 706

RESULT 10
 A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1998 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RP TISSUE-Brain;
 RC MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilblich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11 ALPHA, BETA, AND GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC -----
 DR EMBL, X07648; CAA30488.1; -;
 DR EMBL, X14066; CAA32229.1; -;
 DR PIR, S00550; S00550.
 DR PIR, S03607; S03607.
 DR InterPro, IPR001868; A4_APP.
 DR InterPro, IPR002223; Kunitz_BPTI.
 DR Pfam, PF02177; A4_EXTRA.1.
 DR Pfam, PF00014; Kunitz_BPTI.1.
 DR PRINTS, PR00203; AMYLOIDA4.
 DR PRINTS, PR00204; BETAMAMLOID.
 DR PRINTS, PR00759; BASICPTASE.
 DR SMART, SM00006; A4_EXTRA.1.

DR SMART, SM00131; KU; 1.
 DR PROSITE, PS00319; A4_EXTRA.1.
 DR PROSITE, PS00320; A4_INTRA.1.
 DR PROSITE, PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE, PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPPLIC 269 289
 FT VARSPPLIC 290 364
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B82D929A7 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIIGLM 11
 |||||
 DB 696 GSNKGAIIIGLM 706

RESULT 11
 DDPG_ECOLI STANDARD; PRT; 300 AA.
 ID DPG_ECOLI
 AC P37315;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPGC.
 GN DPGC OR B3542 OR 24959 OR ECS4422.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MMS50;
 RX MEDLINE=95231288; PubMed=7536291;
 RA Abouhamed W.N., Manson M.D.;
 RT "The dipeptide permease of Escherichia coli closely resembles other
 RT bacterial transport systems and shows growth-phase-dependent
 RT expression.";
 RL Mol. Microbiol. 14:1077-1092(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=94316500; PubMed=8041620;
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
 RT Nucleic Acids Res. 22:2576-2586(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoumis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tode T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR DIPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF
CC THE SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: L08399; AAA3704.1; -;
DR EMBL: U00039; AAB18520.1; -;
DR EMBL: AE000431; AAC76567.1; -;
DR EMBL: AE005580; AAG58686.1; -;
DR EMBL: AP002565; BAB37845.1; -;
DR EcoGene: EGI2626; dppc.
DR InterPro: IPR000515; BPD.transp.
DR Pfam: PF00528; BPD.transp.
DR PROSITE: PS00402; BPD.TRANSF.INN_MEMBER_FALSE_NEG.
KW TRANSPORT; Peptide transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 102 122 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 207 227 POTENTIAL.
FT TRANSMEM 231 251 POTENTIAL.
FT TRANSMEM 266 286 POTENTIAL.
SQ SEQUENCE 300 AA; 32308 MW; C4DD7BD82286E62 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 300;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91232862; PubMed=2030914;
RA Blake T.J., Shapiro M., Morse H.C. III, Langdon W.Y.;
RT "The sequences of the human and mouse c-cbl proto-oncogenes show
RT v-cbl was generated by a large truncation encompassing a proline-rich
RT domain and a leucine zipper-like motif."
RL Oncogene 6:653-657(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 47-350.
RX MEDLINE=99176421; PubMed=10078535;
RA Meng W., Sawasdi Kosol S., Burakoff S.J., Eck M.J.;
RT "Structure of the amino-terminal domain of Cbl complexed to its
RT binding site on ZAP-70 kinase."
RL Nature 398:84-90(1999).
CC -1- FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC
CC CELLS. ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR OF
CC MANY SIGNALING PATHWAYS THAT START FROM RECEPTORS AT THE CELL
CC SURFACE.
CC -1- SUBUNIT: ASSOCIATES WITH NCK VIA ITS SH3 DOMAIN.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- PTM: PHOSPHORYLATED ON TYROSINE.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.
CC -----
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CC -----
DR EMBL: X57110; CAA40393.1; -;
DR PIR: A43817; A43817.
DR PDB: 1B47; 27-APR-99.
DR IPI: 165360; -;
DR InterPro: IPR003153; Cbl_N.
DR InterPro: IPR000449; UBA.
DR InterPro: IPR001841; ZnF_Fing.
DR Pfam: PF02262; Cbl_N; 1.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
KW Proto-oncogene; Nuclear protein; Zinc-finger; Phosphorylation;
KW 3D-structure.
FT DOMAIN 124 127 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 381 419 RING-TYPE.
FT DOMAIN 357 476 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 477 688 PRO-RICH.
FT DOMAIN 689 834 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 856 895 UBA.
FT MOD_RES 700 700 PHOSPHORYLATION.
FT MOD_RES 774 774 PHOSPHORYLATION.
SQ SEQUENCE 906 AA; 99646 MW; 7D686B050204AD8F CRC64;

Query Match 68.5%; Score 37; DB 1; Length 906;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;


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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S1 HOMOLOG B.
GN RPS1B OR SUR1984.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: BINDS MRNA.
CC -1- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 'S1 MOTIF' DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90912; BAA18228.1; .
DR HSSP: P05055; ISRO.
DR InterPro: IPR003029; S1.
DR Pfam: PF00575; S1; 3.
DR SMART: SM00316; S1; 3.
KW Ribosomal protein; Repeat; RNA-binding; Complete proteome.
FT REPEAT 29 98 S1 MOTIF 1.
FT REPEAT 116 180 S1 MOTIF 2.
FT REPEAT 194 262 S1 MOTIF 3.
SQ SEQUENCE 305 AA; 33795 MW; 358C35F778BE03F5 CRC64;

Query Match
Best Local Similarity 66.7%; Score 36; DB 1; Length 305;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GSNKGAIG 9
Db 125 GTNKGVG 133

RESULT 14
CBL_MLYCN STANDARD; PRT; 390 AA.
AC P23092;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE TRANSFORMING PROTEIN CBL.
GN V-CBL.
OS Cas-NS-1 murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11793;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89145204; PubMed=2784003;
RA Landon W.Y., Hartley J.W., Klinken S.P., Ruscetti S.K.,
RA Morse H.C. III;
RT "v-cbl, an oncogene from a dual-recombinant murine retrovirus that
RT induces early B-lineage lymphomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1168-1172(1989).

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CC -1- DISEASE: CBL INDUCES EARLY B-LINEAGE LYMPHOMAS.
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-CBL
CC POLYPEPTIDE.
CC -----
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CC -----
DR EMBL: J04169; AAA42885.1; ALT_INIT.
DR PIR: B32325; TVMVCB.
DR InterPro: IPR003153; CBL_N.
DR Pfam: PF02262; Cbl_N; 1.
KW Transforming protein; Oncogene.
SQ SEQUENCE 390 AA; 43692 MW; EB72483746827AB0 CRC64;

Query Match
Best Local Similarity 66.7%; Score 36; DB 1; Length 390;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GSNKGAIGLM 11
Db 50 GSGAGGLIGLM 60

RESULT 15
MGLA_TREPA STANDARD; PRT; 496 AA.
AC 056342;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GALACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA HOMOLOG.
GN MGLA OR TP0685.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97080510; PubMed=8921855;
RA Porcella S.F., Popova T.G., Hagman K.E., Penn C.W., Radolf J.D.,
RA Norgard M.V.;
RT "A mgl-like operon in Treponema pallidum, the syphilis spirochete.";
RL Gene 177:115-121(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.R., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR GALACTOSIDES. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO
CC THE TRANSPORT SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). MGLA/RBSA SUBFAMILY.
CC -----
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CC -----
DR EMBL; U48416; AAC44585.1; -.
DR EMBL; AE001242; AAC65648.1; -.
DR TIGR; TP0685; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001687; ATP_GTP_A.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Transport; Sugar transport; Membrane; ATP-binding; Complete proteome.
FT NP_BIND 37 44 ATP (POTENTIAL)
SQ SEQUENCE 496 AA; 55191 MW; B6F63D53C5CD1411 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 496;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 KGAIIGLM 11
Db 29 KGAVGSLM 36

Search completed: April 24, 2002, 09:20:39
Job time: 253 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:10 ; Search time 62.94 Seconds
(without alignments)
25.564 Million cell updates/sec

Title: US-09-689-469-4
Perfect score: 54
Sequence: 1 GSNKGATIGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTEMBL_17:*
2: sp-archaea:*
3: sp-bacteria:*
4: sp-fungi:*
5: sp-human:*
6: sp-invertebrate:*
7: sp-mhc:*
8: sp-organellar:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	49	6	097917 bos taurus
2	54	100.0	79	11	035463 cricetus
3	54	100.0	82	4	P78438
4	54	100.0	82	4	Q16014
5	54	100.0	82	4	Q16019
6	54	100.0	82	4	Q16020
7	54	100.0	97	4	Q13778
8	54	100.0	534	13	093296
9	54	100.0	569	13	093296
10	54	100.0	607	11	099K32
11	54	100.0	693	11	098K32
12	54	100.0	695	11	098S60
13	54	100.0	695	11	060496
14	54	100.0	695	13	09DGJ8
15	54	100.0	695	13	098SF9
16	54	100.0	699	13	057394
17	54	100.0	737	13	093279
18	54	100.0	747	13	091963
19	54	100.0	751	13	09DGJ7

20	54	100.0	770	6	09TU10	09TU10 sus scrofa
21	54	100.0	780	13	073683	073683 tetradon f
22	48	88.9	612	13	0919E7	0919E7 brachydanio
23	45	83.3	33	4	09UC33	09UC33 homo sapien
24	41	75.9	247	2	09K8R2	09K8R2 bacillus ha
25	39	72.2	296	2	09AE43	09AE43 rhizobium l
26	38	70.4	229	3	007937	007937 bacillus su
27	37	68.5	173	5	09NN73	09NN73 leishmania
28	37	68.5	216	5	010910	010910 caenorhabdi
29	36	66.7	217	9	038156	038156 enterobacte
30	36	66.7	417	2	P71757	P71757 mycobacteri
31	36	66.7	456	2	09RDF0	09RDF0 streptomyce
32	36	66.7	496	2	056341	056341 treponema p
33	35	64.8	203	8	079624	079624 sarcodon im
34	35	64.8	235	11	09DP62	09DP62 mus musculu
35	35	64.8	238	2	066729	066729 aquilex aeo
36	35	64.8	270	11	09D794	09D794 mus musculu
37	35	64.8	270	11	09DP60	09DP60 mus musculu
38	35	64.8	270	11	09C0X3	09C0X3 mus musculu
39	35	64.8	309	2	09RS04	09RS04 delinococcus
40	35	64.8	414	4	013148	013148 homo sapien
41	35	64.8	486	2	033206	033206 mycobacteri
42	35	64.8	509	2	09AP71	09AP71 uncultured
43	35	64.8	515	5	09VJ10	09VJ10 drosophila
44	35	64.8	593	10	09FRL7	09FRL7 arabidopsis
45	35	64.8	673	2	007178	007178 mycobacteri

ALIGNMENTS

```

RESULT 1
097917 ID 097917 PRELIMINARY; PRT: 49 AA.
AC 097917;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANELOID PRECURSOR PROTEIN (FRAGMENT).
GN APP.
OS Bos taurus (Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Re-sequencing of DNA from a diverse panel of cattle reveals frequent
RT polymorphisms in both intron and exon 1";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133033; CAB38017.1; -.
DR HSSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 100.0%; Score 54; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11
Db 8 GSNKGATIGLM 18

RESULT 2
035463 ID 035463 PRELIMINARY; PRT: 79 AA.
AC 035463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

```

DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).
 GN BETA APP.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1; -
 DR HSSP; P05067; 10CM.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2CC63BFF3F597 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 79;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 45 GSNKGAIIGLM 55
 RESULT 3
 ID P78438 PRELIMINARY; PRT; 82 AA.
 AC P78438;
 DT 01-MAY-1997 (TREMURel. 03, Created)
 DT 01-MAY-1997 (TREMURel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
 GN APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [2]
 RP SEQUENCE OF 19-48 FROM N.A.
 RA MEDLINE=87120329; PubMed=2949367;
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
 RT linkage near the Alzheimer locus."
 RL Science 235:880-884(1987).
 RN [3]
 RP SEQUENCE OF 32-63 FROM N.A.
 RA MEDLINE=93035397; PubMed=1415269;
 RA Kamino K., Orr H.T., Payami H., Wlismann E.M., Alonso M.E., Pulst S.M.,
 RA Anderson L., O'dahl S., Nemens E., White J.A.;
 RT "Linkage and mutational analysis of familial Alzheimer disease
 RT kindreds for the APP gene region."
 RL Am. J. Hum. Genet. 51:998-1014(1992).
 DR EMBL; M29270; AAAS1768.1; -
 DR EMBL; M29269; AAAS1768.1; JOINED.
 DR EMBL; M15532; AAAS1564.1; -
 DR EMBL; S45136; AAB23646.1; -
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 41 GSNKGAIIGLM 51

RESULT 4
 ID Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenczwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S60721; AAB26263.2; -
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0095;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 42 GSNKGAIIGLM 52

RESULT 5
 ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenczwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61380; AAB26264.2; -
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
Db 42 GSNKGATIGLM 52

RESULT 6

ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB2625.2; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
Db 42 GSNKGATIGLM 52

RESULT 7

ID Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
FT NON_TER 1
FT 97
SQ SEQUENCE 97 AA; 10884 MW; E528CDB48DE474E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
Db 23 GSNKGATIGLM 33

RESULT 8

ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for Caspase 3 in dying motoneurons.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT 534
SQ SEQUENCE 534 AA; 60597 MW; FB33ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11
|||||
Db 460 GSNKGATIGLM 470

RESULT 9

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RC Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE: P500319; A4_EXTRA; 1.
 DR PROSITE: P500320; A4_INTRA; 1.
 FT NON_TER
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B8B51863A19D CRC64;

Query Match 100.0%; Score 54; DB 13; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 496 GSNKGAIIGLM 506

RESULT 10
 ID Q99K32 PRELIMINARY; PRT; 607 AA.
 AC Q99K32;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005490; AAB05490.1; -.
 FT NON_TER
 SQ SEQUENCE 607 AA; 68391 MW; BF80214CBA7D172 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 533 GSNKGAIIGLM 543

RESULT 11
 ID Q98SG0 PRELIMINARY; PRT; 693 AA.
 AC Q98SG0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BETA-AMYLID PRECURSOR PROTEIN A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001). Department of Biological Sciences,
 University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ296150; CAC37193.1; -.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 693 AA; 78568 MW; CAFIDF555C1AB653 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 693;
 Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GSNKGAIIGLM 11
 DB 619 GSNKGAIIGLM 629

RESULT 12
 ID P97487 PRELIMINARY; PRT; 695 AA.
 AC P97487; P97942;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HIPPOCAMPAL AMYLOID PROTEIN.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SAMP8; TISSUE=HIPPOCAMPUS;
 RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 581-662 FROM N.A.

RC STRAIN-129SV;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capocchi M.,
 RA Loring J.F., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U84012; AAB41502.1; -.
 DR EMBL: U82624; AAB40919.1; -.
 DR HSP: P05067; 10CM.
 DR MGD: MGI:88059; App.
 DR Interpro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: P500319; A4_EXTRA; 1.
 DR PROSITE: P500320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 100.0%; Score 54; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 DB 621 GSNKGAIIGLM 631

RESULT 13
 ID Q60496 PRELIMINARY; PRT; 695 AA.
 AC Q60496;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_Taxid=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Beck M., Mueller D., Bigl V.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O).

CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
 DR EMBL: X97631; CAA66230.1; -
 DR HSSP: P05067; IBA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 54; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 |||
 DB 621 GSNKGAIIGLM 631

RESULT 14

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF289218; AAC00593.1; -
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 |||
 DB 621 GSNKGAIIGLM 631

RESULT 15

ID Q98SF9 PRELIMINARY; PRT; 695 AA.
 AC Q98SF9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN B.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ298151; CAC37194.1; -
 KW SIGNAL.
 FT SIGNAL. 1
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 100.0%; Score 54; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11
 |||
 DB 621 GSNKGAIIGLM 631

Search completed: April 24, 2002, 09:20:11
 Job time: 240 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:50 ; Search time 66.52 Seconds
(without alignments)
33.406 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 30
Sequence: 1 AQNITARIGEPVLKCKGAPKKPPQRLWK 30

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.1101.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	20	AAV09349 Human RAGE V-domain
2	30	100.0	30	21	AAV52134 Human Receptor to
3	30	100.0	318	18	AAW44200 Human mature recep
4	30	100.0	318	18	AAW33754 Human RAGE polypep
5	30	100.0	332	21	AAV52130 Human Receptor to
6	30	100.0	340	18	AAW44199 Human soluble rece
7	30	100.0	340	18	AAW33753 Human RAGE polypep
8	30	100.0	404	22	AAW44192 Extracellular cit
9	16	53.3	16	18	AAW44214 Human soluble RAGE
10	16	53.3	16	18	AAW33768 Human RAGE polypep
11	15	50.0	15	18	AAW44208 Human soluble RAGE

12	15	50.0	15	18	AAW33762	Human RAGE polypep
13	13	43.3	30	20	AAV09350	Mouse RAGE V-domain
14	11	36.7	30	20	AAV09351	Rat RAGE V-domain
15	10	33.3	10	18	AAW44209	Human soluble RAGE
16	10	33.3	10	18	AAW44201	Human soluble RAGE
17	10	33.3	10	18	AAW33763	Human RAGE polypep
18	10	33.3	10	18	AAW33755	Human RAGE polypep
19	10	33.3	10	20	AAV09353	Human RAGE V-domain
20	10	33.3	10	20	AAV52135	Human Receptor to
21	10	33.3	30	20	AAV09352	Bovine RAGE V-domain
22	9	30.0	30	18	AAW23337	N-terminal sequenc
23	7	23.3	178	22	AAW36499	Acinetobacter sp.
24	6	20.0	10	18	AAW27362	Residues 138-147 o
25	6	20.0	10	20	AAW92647	Human HAI-1 peptid
26	6	20.0	49	22	AAW36735	Peptide #10772 enc
27	6	20.0	105	21	AAW57767	Arabidopsis thalia
28	6	20.0	116	21	AAW41577	Human tumour antiq
29	6	20.0	155	21	AAW22865	Murine phosphatase
30	6	20.0	155	21	AAW54142	Arabidopsis thalia
31	6	20.0	160	21	AAW22864	Arabidopsis thalia
32	6	20.0	160	21	AAW54141	Arabidopsis thalia
33	6	20.0	213	19	AAW60564	Human tumour antiq
34	6	20.0	218	22	AAW73217	Murine phosphatase
35	6	20.0	369	16	AAW52004	Arabidopsis thalia
36	6	20.0	399	16	AAW71032	G protein protein
37	6	20.0	400	21	AAW52003	Arabidopsis thalia
38	6	20.0	415	22	AAW85144	Human NKCR polypep
39	6	20.0	422	21	AAW52002	Arabidopsis thalia
40	6	20.0	456	21	AAW20758	Arabidopsis thalia
41	6	20.0	456	21	AAW50449	Arabidopsis thalia
42	6	20.0	481	16	AAW71033	G protein protein
43	6	20.0	481	19	AAW40814	Human 5-Hr2B recep
44	6	20.0	481	21	AAW20757	Arabidopsis thalia
45	6	20.0	481	21	AAW50448	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV09349	AAV09349 standard; peptide: 30 AA.
ID	AAV09349:
XX	09-JUL-1999 (first entry)
XX	Human RAGE V-domain peptide SEQ ID NO:1.
XX	RAGE: V-domain; receptor for advanced glycation endproduct;
KW	ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
KW	senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
KW	neuronal cytotoxicity; head trauma; autoimmune lateral sclerosis;
KW	multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
KW	tumour; cancer; male impotence; wound healing; periodontal disease;
KW	neuropathy; retinopathy; nephropathy; neuronal degeneration.
XX	
OS	Homo sapiens.
XX	
PN	W0918987-A1.
XX	
PD	22-APR-1999.
XX	
PF	09-OCT-1998; 98WC-US21346.
XX	
PR	09-OCT-1997; 97US-0948131.
XX	
PA	(UYCO) UNIV COLUMBIA NEW YORK.
XX	
PI	Iamster I, Schmidt AM, Stern D, Yan SD;
XX	WPI; 1999-277439/23.
DR	
XX	

PT New peptides based on an advanced glycation end product receptor are
PT useful for treating Alzheimer's disease and Down's syndrome
XX
PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
CC amino acid sequence corresponding to an amino acid sequence of a
CC V-domain of a receptor for an advanced glycation end product (RAGE).
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
CC (ABP) interaction with a receptor for RAGE when the receptor is on the
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
CC extracellular assembly of an ABP into a fibril; (5) inhibiting
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
CC of a microglial cell into senile plaques; (7) inhibiting activation of a
CC microglial cell by an ABP; (8) treating a subject with a condition
CC associated with an interaction of an ABP with a receptor for RAGE on a
CC cell; (9) evaluating the ability of an agent to inhibit binding of an
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
CC with a receptor for RAGE when the receptor is on the surface of a cell;
CC and (13) treating a subject with a condition associated with an
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
CC can be used for treating conditions associated with an interaction of an
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
CC disease, senility, renal failure, hyperlipidemic atherosclerosis,
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
CC or neuronal degeneration.
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 4e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKPPQRLWK 30
DB 1 agntarigepvlkckgapkppqrlewk 30

RESULT 2
AAV52134
ID AAV52134 standard; protein; 30 AA.

XX AAV52134;
XX
DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
KM invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble
PT receptor for advanced glycation endproducts -
XX
PS Claim 29; Page 62; 86pp; English.

CC This is the amino acid sequence of a fragment of the human soluble
CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
CC a range of physiologically and pathophysiologically relevant ligands
CC when considering tumour invasion. In normal developing neurons RAGE
CC colocalizes with amphoterin which is a matrix associated polypeptide.
CC The expression of both RAGE and amphoterin decreases after birth, but
CC both have increased expression in tumours. RAGE polypeptides
CC AAV52132-Y52135 are used in the invention in a method for inhibiting
CC tumour invasion and metastasis. The method involves inhibiting tumour
CC invasion and metastasis via administration of a therapeutically effective
CC amount of the pharmaceutical composition containing a RAGE polypeptide.
CC The invention also relates to a method for evaluating the ability of an
CC agent to inhibit tumour invasion in a local cellular environment. RAGE
CC can be administered to a patient in a pharmaceutically acceptable
CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 4e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKPPQRLWK 30
DB 1 agntarigepvlkckgapkppqrlewk 30

RESULT 3
AAW44200
ID AAW44200 standard; Protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;
KM AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 66 /note="encoded by CCR"

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagaishima M;

DR WPI; 1997-558580/51.

DR N-PSDB; AAV12395.

PT Anti-advanced glycosylation end product polypeptide antibody -
PT prevents receptor binding and therefore reduces vascular
PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC carrier.
YY

SQ Sequence 332 AA:

Query Match 100.0%; Score 30; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2,9e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVKCKGAPKPPORLEWK 30
 |||||||
 Db 1 agnitarigeplvIkckgapkppqrlewk 30

RESULT 6
 AAM44199
 ID AAM44199 standard; Protein: 340 AA.

AC AAM44199;

DT 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

KM AGE; antibody; vascular permeability; diabetes mellitus.

XX Homo sapiens.

OS

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PT (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

XX WPI: 1997-558580/51.

DR N-PSDB; AAV12394.

XX Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

XX permeability, useful to treat diabetes mellitus

PS Claim 2; Page 40-41; 90pp; English.

XX The present sequence represents a soluble human receptor to an advanced

CC glycosylation end product (RAGE) polypeptide. The present invention

CC describes an isolated antibody (Ab), specifically immunoreactive with

CC RAGE. Advanced glycosylation end products (AGE) of proteins are

CC non-enzymatically glycosylated proteins, which accumulate in vascular

CC tissue in aging, and at an accelerated rate in individuals with

CC diabetes. The Ab, which prevents the interaction between an AGE and its

CC receptor (RAGE), reduces vascular permeability. The Ab can be used to

CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive

CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis

CC associated amyloidosis or atherosclerosis. The Ab can also be used for

CC the isolation and purification of human RAGE polypeptide.

RESULT 7

AAM33753

AC AAM33753;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;

KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;

XX Alzheimer's disease.

XX Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PT (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

XX WPI: 1997-526458/48.

DR N-PSDB; AAV06517.

XX New soluble advanced glycosylation end-product receptor polypeptide

PT - used for reducing vascular permeability, complications of diabetes

XX etc., also for purification and to screen for modulators

XX Claim 3; Fig 1A; 91pp; English.

PS This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (340 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC are also used, when immobilised, to purify AGE from a protein mixture and

CC to screen for compounds that are agonists and antagonists of AGE/RAGE

CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as

CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of

CC interaction between AGE and RAGE or other receptors and for purification

CC and quantification of RAGE polypeptides. The encoding nucleic acids are

CC used to express recombinant RAGE and as probes for isolating related

CC genes.

SQ Sequence 340 AA:

Query Match 100.0%; Score 30; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 3e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVKCKGAPKPPORLEWK 30
 |||||||
 Db 23 agnitarigeplvIkckgapkppqrlewk 52

RESULT 8
 AAB81925
 ID AAB81925 standard; protein: 404 AA.

```

XX AAB81925;
AC
XX
XX 15-JUN-2001 (first entry)
DT
XX
DE Extracorporeal circulation material receptor protein.
XX
XX Extracorporeal circulation; carbonyl stress product; receptor;
KW diabetes; vascular lesion; excretory dysfunction.
XX
XX unidentified.
OS
XX
XX WO200118060-A1.
PN
XX
XX 15-MAR-2001.
PD
XX
XX 08-SEP-2000; 2000WO-JP06172.
PF
XX
XX 08-SEP-1999; 99JP-0254463.
PR
XX
XX (TORA ) TORAY IND INC.
PA
XX
XX Shimizu S, Kubota M, Akiyama H, Usui M;
PI WPI; 2001-290314/30.
DR
XX
XX Material for extracorporeal circulation, applicable in selective
PT elimination of diabetic complication factors such as carbonyl stress
PT products caused by abnormally promoted carbonyl stress from excretory
PT dysfunction in vascular lesions
PS
XX
XX Claim 1: Page 31-32; 36pp; Japanese.
PS
XX
XX The present invention describes a material for extracorporeal circulation
CC which is made from a water-insoluble carrier immobilized with a protein
CC having the sequence shown here. The materials of the invention, including
CC adsorbents, are for extracorporeal circulation, which are applicable in
CC the selective elimination of diabetic complication factors from a body
CC fluid, and are therefore useful in treating vascular lesions like
CC arteriosclerosis due to carbonyl stress products caused by abnormally
CC promoted carbonyl stress from excretory dysfunction.
CC
XX
XX Sequence 404 AA;
SQ

```

Query Match 100.0%; Score 30; DB 22; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.4e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AONTARIGEPVLKCKGAPKKRPQRLWK 30
   |||||||
DB 23 agnitarigepvlkckgkppqrlwkw 52

```

RESULT 9
 AAW44214
 ID AAW44214 standard; peptide; 16 AA.
 AC AAW44214;
 XX
 XX 14-MAY-1998 (first entry)
 DT
 XX
 XX Human soluble RAGE immunologically active fragment SEQ ID NO.18.
 DE
 XX Human; soluble receptor; advanced glycosylation end product; RAGE;
 KW AGE; antibody; vascular permeability; immunologically active fragment;
 KW diabetes mellitus.
 XX
 XX Homo sapiens.
 OS
 XX WO9739125-A1.
 PN
 XX 23-OCT-1997.
 PD

```

XX
XX 11-APR-1997; 97WO-EP01834.
PF
XX
XX 16-APR-1996; 96US-0633148.
PR
XX
XX (SCHD ) SCHERING PATENTE AG.
PA
XX
XX Hollander DA, Morser MJ, Nagashima M;
PI WPI; 1997-558580/51.
DR
XX
XX Anti-advanced glycosylation end product polypeptide antibody
PT prevents receptor binding and therefore reduces vascular
PT permeability, useful to treat diabetes mellitus
PT
XX
XX Claim 2; Page 49; 90pp; English.
PS
XX
XX The present sequence represents an immunologically active fragment
CC of a soluble human receptor to an advanced glycosylation end
CC product (RAGE) polypeptide. The present invention describes
CC an isolated antibody (Ab), specifically immunoreactive with
CC RAGE. Advanced glycosylation end products (AGE) of proteins are
CC non-enzymatically glycosylated proteins, which accumulate in vascular
CC tissue in ageing, and at an accelerated rate in individuals with
CC diabetes. The Ab, which prevents the interaction between an AGE and it's
CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
CC associated amyloidosis or arteriosclerosis. The Ab can also be used for
CC the isolation and purification of human RAGE polypeptide.
CC
XX
XX Sequence 16 AA;
SQ

```

Query Match 53.3%; Score 16; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e-10;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AONTARIGEPVLKCK 16
   |||||||
DB 1 agnitarigepvlkck 16

```

RESULT 10
 AAW33768
 ID AAW33768 standard; peptide; 16 AA.
 AC AAW33768;
 XX
 XX 08-MAY-1998 (first entry)
 DT
 XX
 XX Human RAGE polypeptide fragment 14.
 DE
 XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; arteriosclerosis;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX WO9739121-A1.
 PN
 XX 23-OCT-1997.
 PD
 XX 11-APR-1997; 97WO-EP01832.
 PF
 XX 16-APR-1996; 96US-0633147.
 PR
 XX (SCHD) SCHERING AG.
 PA
 XX Morser MJ, Nagashima M;
 PI WPI; 1997-526458/48.
 DR
 XX

PT New soluble advanced glycosylation end-product receptor polypeptide
PT - used for reducing vascular permeability, complications of diabetes
PT etc., also for purification and to screen for modulators
XX
PS Disclosure: Page 9, 91pp; English.

This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active fragments or their mimetics can inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus or occlusive vascular complications such as micro- or macro- vasculopathy (particularly retinopathy) or neuropathy, nephropathy, atherosclerosis or rheinopathy) or haemodialysis-associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related genes.

50 Sequence 16 AA;

Query Match	53.3%	Score 16;	DB 18;	Length 16;
Best Local Similarity	100.0%	Pred. No. 2e-10;		
Matches 16; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

```
Qy 1 AQNTARIGEPLVLC 16
    111111111111111
Db 1 agnitarigeplv1kc 16
```

RESULT	ID
11	AAW44208
	standard; peptide; 15 AA.

AC	AAW44208;
XX	
DT	14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:12.

KM Human; soluble receptor; advanced glycosylation end product; RAGE;
KM AGE; antibody; vascular permeability; immunologically active fragment;
KM diabetes mellitus.

OS Homo sapiens

PN W09739125-A1

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M,

DR WPI; 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody

PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 46; 90pp; English.

CC The present sequence represents an immunologically active fragment
CC of a soluble human receptor to an advanced glycosylation end
CC product (AGE) polypeptide. The present invention describes
CC an isolated antibody (Ab), specifically immunoreactive with
CC AGE. Advanced glycosylation end products (AGE) of proteins are
CC non-enzymatically glycosylated proteins, which accumulate in vascular
CC tissue in ageing, and at an accelerated rate in individuals with
CC diabetes. The Ab, which prevents the interaction between an AGE and its
CC receptor (AGE), reduces vascular permeability. The Ab can be used to
CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
CC associated amyloidosis or atherosclerosis. The Ab can also be used for
CC the isolation and purification of human AGE polypeptide.

50 Sequence 15 AA;

Query Match	50.0%	Score 15;	DB 18;	length 15;
Best Local Similarity	100.0%;	Pred. No.	2.2e-09;	
Matches 15; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```
QY      1 AONITARIGEPLVK 15
        |||||
Db      1 agnitarigeplvk 15
```

RESULT	12
AAW33762	
ID	AAW33762 standard; peptide; 15 AA

AC	AAW33762;
XX	
DT	08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 8

KM Advanced glycosylation end-product receptor; RAGE; screening; AGE;
KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;
KM Alzheimer's disease.

OS Homo sapiens.

PN W09739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

PT New soluble advanced glycosylation end-product receptor polypeptide

PT etc., also for purification and to screen for modulators

PS Claim 6; Page 55; 91pp; English

CC This is a peptide fragment of a human advanced glycosylation end-product

CC fragments or their mimetics can inhibit interaction between advanced glycation end products (AGE) and a receptor (specifically RAGE) thereby

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC complications such as micro- or macro-vascular pathology or occlusive vascular

CC retinopathy) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.

XX Sequence 15 AA;

Query Match 50.0%; Score 15; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred.No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQNTARIGEPLVLK 15
 DB 1 agntarigeplvlk 15

RESULT 13

AA09350
 ID AAY09350 standard; peptide: 30 AA.

XX AAY09350;

XX 09-JUL-1999 (first entry)

DE Mouse RAGE V-domain peptide SEQ ID NO:2.

XX RAGE; V-domain; receptor for advanced glycation endproduct;
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW tumour; cancer; male impotence; wound healing; periodontal disease;
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

XX Mus sp.

XX WO918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

XX WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are
 PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 3; Page 78; 101pp; English.

XX The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a

CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.

XX Sequence 30 AA;

Query Match 43.3%; Score 13; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred.No. 5.2e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGEPLVL 14
 DB 2 qntarigeplvl 14

RESULT 14

AA09351
 ID AAY09351 standard; peptide: 30 AA.

XX AAY09351;

XX 09-JUL-1999 (first entry)

DE Rat RAGE V-domain peptide SEQ ID NO:3.

XX RAGE; V-domain; receptor for advanced glycation endproduct;
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW tumour; cancer; male impotence; wound healing; periodontal disease;
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

XX Rattus sp.

XX WO918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

XX WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are
 PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 4; Page 78; 101pp; English.

XX The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide

CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 CC
 SQ Sequence 30 AA;

Query Match 36.7%; Score 11; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.1e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPV 12
 |||||
 Db 2 qntarigepl 12

RESULT 15
 AAM44209

ID AAM44209 standard; peptide; 10 AA.

AC AAM44209;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:13.

KM Human: soluble receptor; advanced glycosylation end product; RAGE;

KW AGE; antibody; vascular permeability; immunologically active fragment;
 diabetes mellitus.

OS Homo sapiens.

PN WC9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

WPI; 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

PS permeability, useful to treat diabetes mellitus

CC Claim 2; Page 47; 90pp; English.
 CC The present sequence represents an immunologically active fragment

CC of a soluble human receptor to an advanced glycosylation end
 CC product (RAGE) polypeptide. The present invention describes
 CC an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.
 CC
 SQ Sequence 10 AA;

Query Match 33.3%; Score 10; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKKRPQ 25
 |||||
 Db 1 ckgapkxrpq 10

Search completed: April 24, 2002, 09:21:51
 Job time: 250 sec

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Db 1 AONITARIGEPVLKCKGAPKPPORLEWK 30

RESULT 2

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSEY, MICHAEL J.

APPLICANT: MAGASHIMA, NARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-00560005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-2

Query Match 100.0%; Score 30; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 1.3e-24;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGEPVLKCKGAPKPPORLEWK 30

Db 23 AONITARIGEPVLKCKGAPKPPORLEWK 52

RESULT 3

US-08-432-016-5

Sequence 5, Application US/08432016

Patent No. 5968768

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,016

FILING DATE: 01-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903

FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-016-5

Query Match 76.7%; Score 23; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLKCKGAPKPPORLEWK 30

Db 1 IGEPLVLKCKGAPKPPORLEWK 23

RESULT 4

US-08-684-594-5

Sequence 5, Application US/08684594

Patent No. 5998172

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594

FILING DATE: 18-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016

APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-00560005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ. ID NO: 5:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-5

Query Match 33.3%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKPKQ 25
DB 1 CKGAPKPKQ 10

RESULT 8
US-08-633-148-13
Sequence 13, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-00560005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-13

Query Match 33.3%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKPKQ 25
DB 1 CKGAPKPKQ 10

RESULT 9
US-08-685-558A-2
Sequence 2, Application US/08685558A
Patent No. 6225081
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
US-08-685-558A-2

Query Match 20.0%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EPLVLK 15
|||||
DB 5 EPLVLK 10

RESULT 10
US-08-416-788-2

; Sequence 2, Application US/08416788
; Patent No. 5780245

; GENERAL INFORMATION:

; APPLICANT: Marcoux, Luc

; TITLE OF INVENTION: No. 5780245el Polypeptides Having a Serotonin

; TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcoia Road, 3043

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/416,788

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/FR93/01012

; FILING DATE: 13-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92-12280

; FILING DATE: 14-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Julie K.

; REGISTRATION NUMBER: 38,619

; REFERENCE/DOCKET NUMBER: EX92008-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610)454-3839

; TELEFAX: (610)454-3808

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 479 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-416-788-2

OY 22 KPPQRL 27

|||||
DB 253 KPPQRL 258

RESULT 11
US-08-173-436A-2

; Sequence 2, Application US/08173436A

; Patent No. 5698444

; GENERAL INFORMATION:

; APPLICANT: Baez, Melvyn

; TITLE OF INVENTION: SEROTONIN RECEPTOR PROTEIN AND RELATED

; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN

; COUNTRY: US

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/173,436A

; FILING DATE: 23-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Gaylo, Paul J.

; REGISTRATION NUMBER: 36,808

; REFERENCE/DOCKET NUMBER: X-9367

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-0756

; TELEFAX: 317-276-3861

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 481 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-173-436A-2

OY 22 KPPQRL 27

|||||
DB 254 KPPQRL 259

RESULT 12
US-08-748-485-8

; Sequence 8, Application US/08748485

; Patent No. 5817480

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice

; APPLICANT: Guegler, Karl J.

; APPLICANT: Goli, Surya K.

; APPLICANT: Murry, Lynn E.

; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: US

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/748,485

; FILING DATE: Herewith

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0159 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 475198
US-08-748-485-8

Query Match 20.0%; Score 6; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KPPORL 27
Db 254 KPPORL 259

RESULT 13
US-08-685-558A-18
Sequence 18, Application US/08665558A
Patent No. 6225081
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
US-08-685-558A-18

Query Match 20.0%; Score 6; DB 4; Length 513;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPLVLK 15
Db 177 EPLVLK 182

RESULT 14
US-08-277-231A-4
Sequence 4, Application US/08277231A
Patent No. 5643725
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pili
Patent No. 5643725
TITLE OF INVENTION: Structural Genes and The LKP Pili Operon of No. 5643725type
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,231A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 32,542
REFERENCE/DOCKET NUMBER: ACC94-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-277-231A-4

Query Match 20.0%; Score 6; DB 1; Length 741;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
Db 157 TARIGE 162

RESULT 15
US-08-473-750-7
Sequence 7, Application US/08473750
Patent No. 5834187
Patent No. 5834187 5786143
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pili
Patent No. 5834187
Patent No. 5834187 5786143
TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. 5834187 5786
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,321
FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-750-7

Query Match 20.0%; Score 6; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

OY 5 TARIGE 10
| | | | |
Db 157 TARIGE 162

Search completed: April 24, 2002, 09:22:30
Job time: 249 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:16 ; Search time 38.65 seconds
(without alignments)
59.126 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 30
Sequence: 1 AQNITARIGEPVLKCKGAPKPPQRLKWK 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	404	1	I61596 advanced glycosyla
2	13	43.3	402	1	T09062 probable advanced
3	10	33.3	416	1	A42879 advanced glycosyla
4	7	23.3	223	2	H64065 mutator muth - Hae
5	7	23.3	330	2	E81998 pseudouridylylate sy
6	7	23.3	330	2	H81225 ribosomal large ch
7	7	23.3	537	1	J01619 cell fusion glycop
8	7	23.3	595	2	B86212 protein F24B9.20 l
9	6	20.0	96	2	T07822 cystein proteinase
10	6	20.0	110	2	S64538 hypothetical prote
11	6	20.0	155	2	T46154 hypothetical prote
12	6	20.0	209	2	E70536 hypothetical prote
13	6	20.0	230	2	A75260 hypothetical prote
14	6	20.0	234	1	Q08E43 membrane antigen g
15	6	20.0	238	2	H64181 ABC-type transport
16	6	20.0	257	2	D70552 hypothetical prote
17	6	20.0	271	2	A70415 mylodopterin bios
18	6	20.0	282	2	T07303 cell division inh
19	6	20.0	298	2	T51746 RNA helicase RH17
20	6	20.0	326	2	H83187 hypothetical prote
21	6	20.0	334	2	D83164 conserved hypotet
22	6	20.0	359	2	T35179 oxidoreductase alp
23	6	20.0	387	2	C96670 hypothetical prote
24	6	20.0	389	2	S33667 probable integrase
25	6	20.0	429	2	T23984 hypothetical prote
26	6	20.0	468	2	H69133 argininosuccinate
27	6	20.0	471	2	S30585 hypothetical prote
28	6	20.0	474	2	B82227 exodeoxyribonuclea
29	6	20.0	479	2	C86275 hypothetical prote

30	6	20.0	481	2	S43687 serotonin receptor
31	6	20.0	481	2	S49442 serotonin receptor
32	6	20.0	504	2	S27269 serotonin receptor
33	6	20.0	509	2	T36710 hypothetical prote
34	6	20.0	511	2	JE0312 3-ketosteroid-deta
35	6	20.0	548	2	T05671 hypothetical prote
36	6	20.0	560	2	T05278 hypothetical prote
37	6	20.0	562	2	T24462 hypothetical prote
38	6	20.0	567	2	A84728 hypothetical prote
39	6	20.0	608	2	C83322 excludinase ABC s
40	6	20.0	609	2	G84832 ATP-dependent RNA
41	6	20.0	635	2	E71733 threonine--trna 11
42	6	20.0	714	2	A70983 probable fusA2 pro
43	6	20.0	748	2	S54505 hypothetical prote
44	6	20.0	754	1	BAB0H peptide-aspartate
45	6	20.0	757	2	I38423 aspartyl beta-hydr

ALIGNMENTS

RESULT 1
I61596
advanced glycosylation end-products receptor precursor - human
N:Alternate names: advanced glycosylation end product-binding protein, 35K, glycoprot
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: I61596; B42879; S27968
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.
Genomics 23, 408-419, 1994
A>Title: Three genes in the human MHC class III region near the junction with the cl
nterpart of mouse mammary tumor gene int-3.
A:Reference number: A55562; MIM:95137587
A:Accession: I61596
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-404 <RES>
A:Cross-references: GB:D28769; NID:q561657; PIDN:BA005958.1; PID:q561659
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A:Reference number: A42879; MIM:92340547
A:Accession: B42879
A:Molecule type: mRNA
A:Residues: 'G', 2-99, 'R', 101-404 <NE>
A:Cross-references: EMBL:M91211; NID:q190845; PIDN:AAA03574.1; PID:q190846
A:Experimental source: Lung
A:Note: sequence extracted from NCBI backbone (NCBI:109438)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Genetics:
A:Gene: GDB:AGER
A:Cross-references: GDB:306354; OMIM:600214
A:Map position: 6p21.3-6p21.3
A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-404/Product: advanced glycosylation end products receptor #status predicted <EXT>
F:23-344/Domain: extracellular #status predicted <EXT>
F:31-101/Domain: immunoglobulin homology <IM1>
F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:345-362/Domain: transmembrane #status predicted <TMW>
F:363-404/Domain: intracellular #status predicted <INT>
F:25,81/Binding site: carbohydrate bonds (covalent) #status predicted
F:38-99,144-208,259-301/Disulfide bonds: #status predicted

Query Match 100.0%; Score 30; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 1.7e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLVKCKGAKRPPORLEWK 30
 DB 23 AONTARIGEPVLVKCKGAKRPPORLEWK 52

RESULT 2
 T09062
 Probable advanced glycosylation end-products receptor precursor - mouse
 N:Alternate names: RAGE
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
 C:Accession: T09062
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahern, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
 submitted to the EMBL Data Library, October 1997
 A:Description: Sequence of the mouse major histocompatibility locus class III region.
 A:Reference number: Z16543
 A:Accession: T09062
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-402 <ROW>
 A:Cross-references: EMBL:AF030001; NID:92564945; PID:92564950
 C:Genetics: RAGE
 A:Gene: RAGE
 A:Map position: 17
 A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
 C:Superfamily: advanced glycosylation end products receptor; Immunoglobulin homology
 C:Keywords: receptor; transmembrane protein
 F:31-100/Domain: Immunoglobulin homology <IMM>

Query Match 43.3%; Score 13; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGEPLVL 14
 DB 24 QNTARIGEPLVL 36

RESULT 3
 A42879
 Advanced glycosylation end-products receptor precursor - bovine
 N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
 C:Accession: A42879; A42878; S27949
 R:Keeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
 J. Biol. Chem. 267, 14998-15004, 1992
 A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
 A:Reference number: A42879; MUID:92340547
 A:Accession: A42879
 A:Molecule type: mRNA
 A:Residues: 1-416 <NDE>
 A:Cross-references: GB:M9212; NID:g163650; PIDN:AAA03575.1; PID:g163651
 A:Experimental source: Lung
 A:Note: sequence extracted from NCBI backbone (NCBI:P.109436)
 A:Note: parts of this sequence, including the amino end of the mature protein, were dete
 R.Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
 J. Biol. Chem. 267, 14987-14997, 1992
 A:Title: Isolation and characterization of two binding proteins for advanced glycosylati
 A:Reference number: A42878; MUID:92340546
 A:Accession: A42878
 A:Molecule type: protein
 A:Residues: 23-24, 'X', '26-37', 'X', '39-49', 'XX', '52-54' <SCH>
 A:Experimental source: endothelial cells
 A:Note: sequence extracted from NCBI backbone (NCBI:P.109434)
 C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
 cellular function, thus contributing to tissue lesions in diabetes.
 C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
 C:Function:
 A:Description: neuronal receptor for amphotericin, a DNA-binding protein involved in ne
 C:Superfamily: advanced glycosylation end products receptor; Immunoglobulin homology
 C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
 F:31-100/Domain: extracellular #status predicted <EXT>
 F:31-100/Domain: Immunoglobulin homology <IM1>
 F:136-209/Domain: Immunoglobulin homology <IM2>
 F:262-313/Domain: Immunoglobulin homology <IM3>
 F:355-372/Domain: transmembrane #status predicted <TM>
 F:373-416/Domain: intracellular #status predicted <INT>
 F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 33.3%; Score 10; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKRPQ 25
 DB 38 CKGAPKRPQ 47

RESULT 4
 H64065
 Mutator muth - Haemophilus influenzae (strain Rd KW20)
 N:Alternate names: DNA mismatch protein
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman
 , D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.W.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:9530630
 A:Accession: H64065
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-223 <TIGR>
 A:Cross-references: GB:U32723; GB:I42023; NID:g1573363; PIDN:AAC22062.1; PID:g1573374
 C:Genetics:
 A:Gene: muth
 C:Superfamily: mutator muth

Query Match 23.3%; Score 7; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ITARIGE 10
 DB 165 ITARIGE 171

RESULT 5
 E81998
 pseudouridylylate synthase (PC 4.2.1.70) C RNA-specific NMA0070 [imported] - Neisseria
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
 A:Reference number: AB1775; MUID:20222556
 A:Accession: E81998
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-330 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83386.1; PID:g737884
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: rLUC; NMA0070
C:Superfamily: conserved hypothetical protein H10176
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 23.3%; Score 7; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPVLK 15
|||||||
DB 304 GEPVLK 310

RESULT 6
H81225
ribosomal large chain pseudouridine synthase C NMB0198 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81225
R:Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: H81225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <TEMP>
A:Cross-references: GB:AE002377; GB:AE002098; NID:g7225416; PIDN:AAF0655.1; PID:g722541
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0198
C:Superfamily: conserved hypothetical protein H10176

Query Match 23.3%; Score 7; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPVLK 15
|||||||
DB 304 GEPVLK 310

RESULT 7
J01619
cell fusion glycoprotein precursor - pneumonia virus of mice
N:Alternate names: F protein
N:Contents: cell fusion glycoprotein F1; cell fusion glycoprotein F2
C:Species: pneumonia virus of mice
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 25-Oct-1996
C:Accession: J01619
R:Chambers, P.; Pringle, C.R.; Easton, A.J.
J. Gen. Virol. 73, 1717-1724, 1992
A:Title: Sequence analysis of the gene encoding the fusion glycoprotein of pneumonia vir
A:Reference number: J01619; MUID:92333256
A:Accession: J01619
A:Molecule type: mRNA
A:Residues: 1-537 <CHN>
A:Cross-references: GB:S40186
C:Genetics:
A:Gene: F
C:Superfamily: cell fusion glycoprotein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-101/Product: cell fusion glycoprotein F2 #status predicted <PG2>

F:102-537/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F:491-514/Domain: transmembrane #status predicted <TRM>
F:463-488/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 23.3%; Score 7; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPVLK 15
|||||||
DB 434 GEPVLK 440

RESULT 8
B86212
protein F24B9.20 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B86212
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: B86212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-595 <STO>
A:Cross-references: GB:AE005172; NID:g8439898; PIDN:AAF75084.1; GSPDB:GN00141
C:Genetics:
A:Gene: F24B9.20
A:Map position: 1

Query Match 23.3%; Score 7; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RICEPLY 13
|||||||
DB 550 RICEPLY 556

RESULT 9
T07822
cystein proteinase inhibitor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C:Accession: T07822
R:Yamakawa, S.
submitted to the EMBL Data Library, May 1998
A:Description: Cystein proteinase inhibitor.
A:Reference number: Z16154
A:Accession: T07822
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <YAM>
A:Cross-references: EMBL:AB014760; PIDN:BAA28867.1
A:Note: root-specific
C:Superfamily: cystatin; cystatin homology
C:Keywords: cysteine proteinase inhibitor

Query Match 20.0%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVLKCK 17
|||||
Db 59 LVLKCK 64

RESULT 10

S64538
hypothetical protein YGR215W - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein G7821

C:Species: Saccharomyces cerevisiae

C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000

C:Accession: S64538

R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996

A:Reference number: S64071

A:Accession: S64538

A:Molecule type: DNA

A:Residues: 1-110 <R1E>

A:Cross-references: EMBL:Z73000; NID:g1323386; PID:g1323387; GSPDB:GN00007; MIPS:YGR215W

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YGR215W

A:Map position: 7R

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YGR215W

Query Match

Best Local Similarity 20.0%; Score 6; DB 2; Length 110;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKK 22
|||||

Db 88 KGAPKK 93

RESULT 11

T46154

hypothetical protein T4D2.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46154

R:Myakura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23025

A:Accession: T46154

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-155 <NYA>

A:Cross-references: EMBL:AL132958

A:Experimental source: cultivar Columbia; BAC clone T4D2

C:Genetics:

A:Map position: 3

A:Introns: 118/3

A:Note: T4D2.10

Query Match

Best Local Similarity 20.0%; Score 6; DB 2; Length 155;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCKGAP 20
|||||

Db 139 KCKGAP 144

RESULT 12

E70536

hypothetical protein RV0804 - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: E70536

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squires, S.
Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the Biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; M0ID:98295987

A:Accession: E70536

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-209 <COL>

A:Cross-references: GB:Z95618; GB:AL123456; NID:g3261788; PIDN:CAB09107.1; PID:e31727

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: RV0804

Query Match

Best Local Similarity 20.0%; Score 6; DB 2; Length 209;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVL 14
|||||

Db 151 GEPLVL 156

RESULT 13

A75260

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: A75260

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

; M.; Shen, M.; Yamathayan, J.J.; Lam, P.; McDonald, L.; Utracki, T.; Zaleski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; M0ID:20036896

A:Accession: A75260

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-230 <WHI>

A:Cross-references: GB:AE002084; GB:AE000513; NID:g6460372; PIDN:AAF12096.1; PID:g646

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2550

A:Map position: 1

Query Match

Best Local Similarity 20.0%; Score 6; DB 2; Length 230;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ARIGEP 11
|||||

Db 121 ARIGEP 126

RESULT 14

Q08543

membrane antigen gp85 - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus

C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999

C:Accession: F43044; A03787; S33040

R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A>Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi

A:Reference number: A93065; M0ID:85035713

A:Accession: F43044

A:Molecule type: DNA

A:Residues: 1-234 <BAN>

A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24835.1; PID:g1334899

R:Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.

Nature 310, 207-211, 1984

A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:8427067
A:Contents: annotation: protein coding region
C:Superfamily: Epstein-Barr virus membrane antigen gp85

Query Match 20.0%; Score 6; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AONITA 6
|||||
Db 108 AONITA 113

RESULT 15

H64181
ABC-type transport system probable membrane spanning protein - Haemophilus influenzae (S
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Aug-1998
C:Accession: H64181
R:Flitschman, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Goearney, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: H64181
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-238 <TIGR>
A:Cross-references: GB:I42023; TIGR:HI1079
C:Superfamily: histidine permease protein M

Query Match 20.0%; Score 6; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6
|||||
Db 195 AONITA 200

Search completed: April 24, 2002, 09:23:17
Job time: 246 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:36 ; Search time 66.28 Seconds
(Without alignments)
33.527 Million cell updates/sec

Title: US-09-689-469-5

Perfect score: 162

Sequence: 1 AONTARICEPLVLCKGAPKPPQRLMK 30

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID8/gcgdata/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/AA1986.DAT.*
8: /SID8/gcgdata/geneseq/AA1987.DAT.*
9: /SID8/gcgdata/geneseq/AA1988.DAT.*
10: /SID8/gcgdata/geneseq/AA1989.DAT.*
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12: /SID8/gcgdata/geneseq/AA1991.DAT.*
13: /SID8/gcgdata/geneseq/AA1992.DAT.*
14: /SID8/gcgdata/geneseq/AA1993.DAT.*
15: /SID8/gcgdata/geneseq/AA1994.DAT.*
16: /SID8/gcgdata/geneseq/AA1995.DAT.*
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18: /SID8/gcgdata/geneseq/AA1997.DAT.*
19: /SID8/gcgdata/geneseq/AA1998.DAT.*
20: /SID8/gcgdata/geneseq/AA1999.DAT.*
21: /SID8/gcgdata/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	30	AA09349	Human RAGE V-domain
2	162	100.0	30	AA52134	Human Receptor to
3	162	100.0	318	AA54200	Human mature recep
4	162	100.0	318	AAW33754	Human RAGE polypep
5	162	100.0	332	AA52130	Human Receptor to
6	162	100.0	340	AAW44199	Human soluble rece
7	162	100.0	340	AAW33753	Human RAGE polypep
8	162	100.0	404	AAW81925	Extracellular cir
9	149	92.0	30	AA09350	Mouse RAGE V-domain
10	145	89.5	30	AA09352	Bovine RAGE V-domain
11	133	82.1	30	AA09351	Rat RAGE V-domain

12	127	78.4	30	AAW23337	N-terminal seque
13	81	50.0	16	AAW44214	Human soluble RAGE
14	81	50.0	16	AAW33768	Human RAGE polypep
15	72	44.4	15	AAW44208	Human soluble RAGE
16	72	44.4	15	AAW33762	Human RAGE polypep
17	60	37.0	10	AAW44209	Human soluble RAGE
18	60	37.0	10	AAW44201	Human soluble RAGE
19	60	37.0	10	AAW33763	Human RAGE polypep
20	60	37.0	10	AAW33755	Human RAGE polypep
21	55.5	34.3	1496	AAW81030	Human RAGE polypep
22	55.5	34.3	1496	AAW70469	Human p53 target m
23	55	34.0	312	AAW50904	Human PRO245 prote
24	54	33.3	602	AAW51705	Neurotrophic facto
25	54	33.3	602	AAW32900	Chicken neurotroph
26	53.5	33.0	767	AAW25696	Human protein sequ
27	53.5	33.0	1101	AAW08008	Human H16-1 prote
28	53	32.7	298	AAW5220	Human secreted pro
29	53	32.7	753	AAW83927	Human T85 protein.
30	53	32.7	1649	AAW08404	Human ROBO1 protel
31	53	32.7	1651	AAW13566	Human Robo 1 polyp
32	52.5	32.4	4412	AAW53666	Sequence g1/101742
33	52	32.1	298	AAW85457	Secreted protein e
34	52	32.1	298	AAW87273	Human confuency r
35	52	32.1	298	AAW37275	Murine confuency r
36	52	32.1	298	AAW00512	Human junctional a
37	52	32.1	303	AAW23693	Human EST encoded
38	52	32.1	312	AAW08060	Human PRO245 prote
39	52	32.1	312	AAW23324	A33 related anti
40	52	32.1	312	AAW13354	Amino acid sequenc
41	52	32.1	312	AAW33421	Human PRO245 prote
42	52	32.1	312	AAW24401	Human PRO245 prote
43	52	32.1	312	AAW70668	Human PRO245 prote
44	52	32.1	312	AAW12339	Human PRO245 polyp
45	52	32.1	312	AAW00821	Human immune respo

ALIGNMENTS

RESULT 1	
AA09349	AA09349 standard; peptide; 30 AA.
XX	XX
XX	XX
AC	AA09349;
XX	XX
DT	09-JUL-1999 (first entry)
XX	XX
XX	XX
DE	Human RAGE V-domain peptide SEQ ID NO:1.
XX	XX
KW	RAGE: V-domain; receptor for advanced glycation endproduct;
KW	ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
KW	senility; renal failure; hyperlipidemic atherosclerosis; dementia;
KW	neuronal cytotoxicity; head trauma; autoimmune lateral sclerosis;
KW	multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
KW	tumour; cancer; male impotence; wound healing; periodontal disease;
KW	neuropathy; retinopathy; nephropathy; neuronal degeneration.
XX	XX
OS	homo sapiens.
XX	XX
PN	WO918987-A1.
XX	XX
PD	22-APR-1999.
XX	XX
PF	09-OCT-1998; 98WO-US21346.
XX	XX
PR	09-OCT-1997; 97US-0948131.
XX	XX
PA	(UYCO) UNIV COLUMBIA NEW YORK.
XX	XX
PI	Lamster I, Schmidt AM, Stern D, Yan SD;
XX	XX
DR	WPI; 1999-277439/23.
XX	XX

PT New peptides based on an advanced glycation end product receptor are
 useful for treating Alzheimer's disease and Down's syndrome
 XX
 PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (Aβ) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an Aβ fibril on a cell; (4) inhibiting
 CC extracellular assembly of an Aβ into a fibril; (5) inhibiting
 CC aggregation of Aβ on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an Aβ; (8) treating a subject with a condition
 CC associated with an interaction of an Aβ with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC Aβ with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC Aβ or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 CC
 SQ Sequence 30 AA:

Query Match 100.0%; Score 162; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.5e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKPPQRLWK 30
 Db 1 agntarigepvlkckgapkppqrlewk 30

RESULT 2

AA52134
 ID AAY52134 standard; protein; 30 AA.

AC AAY52134;
 XX
 DT 28-JAN-2000 (first entry)
 XX

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 invasion; metastasis; amphoterin; neuron; inhiblt; therapy.
 XX
 OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;
 XX
 DR WPI; 2000-013260/01.

XX
 PT Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -
 XX
 PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

SQ Sequence 30 AA:

Query Match 100.0%; Score 162; DB 21; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.5e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKPPQRLWK 30
 Db 1 agntarigepvlkckgapkppqrlewk 30

RESULT 3

AAW44200
 ID AAW44200 standard; Protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)
 XX

DE Human mature receptor to an advanced glycosylation end product.

KW Human: soluble receptor; advanced glycosylation end product; RAGE;
 KM AGE; antibody; vascular permeability; diabetes mellitus.
 XX
 OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT Misc-difference 66 /note="encoded by CCR"

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

XX
 XX
 DR WPI; 1997-558580/51.

DR N-PSDB; AAY12395.

XX
 XX
 PT Anti-advanced glycosylation end product polypeptide antibody -

PT prevents receptor binding and therefore reduces vascular
 permeability, useful to treat diabetes mellitus
 XX
 XX

Claim 2; Page 42-43; 90pp; English.

XX The present sequence represents a mature human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 318 AA:

Query Match 100.0%; Score 162; DB 18; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.7e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKKPPQRLWK 30
 Db 1 aqnlrtarigepvlkckgapkkppqrlewk 30

RESULT 4

AAW33754
 ID AAW33754 standard; Protein; 318 AA.

AC AAW33754;

DT 08-MAY-1998 (first entry)

XX Human RAGE polypeptide (318 amino acid residues).

KM Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 XX Alzheimer's disease.

OS Homo sapiens.

PN W09739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

DR N-PSDB; AAW06518.

XX New soluble advanced glycosylation end-product receptor polypeptide
 PT -used for reducing vascular permeability, complications of diabetes
 PT etc., also for purification and to screen for modulators
 PS Claim 3; Fig 1B; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (318 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.

XX Sequence 318 AA:

Query Match 100.0%; Score 162; DB 18; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.7e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKKPPQRLWK 30
 Db 1 aqnlrtarigepvlkckgapkkppqrlewk 30

RESULT 5

AA52130
 ID AA52130 standard; protein; 332 AA.

AC AA52130;

DT 28-JAN-2000 (first entry)

XX Human Receptor to AGE (RAGE) amino acid sequence.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 KW invasion; metastasis; amphotericin; neuron; inhibit; therapy.

XX Homo sapiens.

PN W09954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -
 PS Disclosure: Page 10-11; 88pp; English.

XX This is the amino acid sequence of the human soluble Receptor for
 CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of
 CC physiologically and pathophysiologically relevant ligands when
 CC considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphotericin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphotericin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AA52132-Y52133 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

SQ Sequence 332 AA;

Query Match 100.0%; Score 162; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2.8e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCCKGAPKPPORLEWK 30
 ||||||||||||||||||||||||||||
 Db 1 agnitarigeplvlckgapkppqrlwkw 30

RESULT 6

AAW44199
 ID AAW44199 standard; Protein; 340 AA.

AC AAW44199;

PD 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

XX AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

XX MO9739125-A1.

XX 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

XX (SCHD) SCHERING PATENTE AG.

PA Hollander DA, Morser MJ, Nagashima M;

PI WPI; 1997-558580/51.

DR N-PSDB; AAV12394.

XX Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

PS permeability, useful to treat diabetes mellitus

XX Claim 2; Page 40-41; 90pp; English.

XX The present sequence represents a soluble human receptor to an advanced

CC glycosylation end product (RAGE) polypeptide. The present invention

CC describes an isolated antibody (Ab), specifically immunoreactive with

CC RAGE. Advanced glycosylation end products (AGE) of proteins are

CC tissue in ageing, and at an accelerated rate in individuals with

CC diabetes. The Ab, which prevents the interaction between an AGE and it's

CC receptor (RAGE), reduces vascular permeability. The Ab can be used to

CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive

CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis

CC associated amyloidosis or atherosclerosis. The Ab can also be used for

CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 340 AA;

Query Match 100.0%; Score 162; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCCKGAPKPPORLEWK 30
 ||||||||||||||||||||||||||||
 Db 23 agnitarigeplvlckgapkppqrlwkw 52

RESULT 7

AAW33753
 ID AAW33753 standard; Protein; 340 AA.

AC AAW33753;

PD 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;

XX vascular permeability; diabetes mellitus; treatment; atherosclerosis;

XX Alzheimer's disease.

XX Homo sapiens.

XX MO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

XX (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

DR N-PSDB; AAV06517.

XX New soluble advanced glycosylation end-product receptor polypeptide

PT - used for reducing vascular permeability, complications of diabetes

XX etc., also for purification and to screen for modulators

XX Claim 3; Fig 1A; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (340 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC are also used, when immobilised, to purify AGE from a protein mixture and

CC to screen for compounds that are agonists and antagonists of AGE/RAGE

CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as

CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of

CC interaction between AGE and RAGE or other receptors and for purification

CC and quantification of RAGE polypeptides. The encoding nucleic acids are

CC used to express recombinant RAGE and as probes for isolating related

SQ Sequence 340 AA;

Query Match 100.0%; Score 162; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCCKGAPKPPORLEWK 30
 ||||||||||||||||||||||||||||
 Db 23 agnitarigeplvlckgapkppqrlwkw 52

RESULT 8

AAW81925
 ID AAW81925 standard; Protein; 404 AA.

```

XX AC AAB81925;
XX XX
XX DT 15-JUN-2001 (first entry)
XX DE Extracorporeal circulation material receptor protein.
XX KM Extracorporeal circulation; carbonyl stress product; receptor;
XX KM diabetes; vascular lesion; excretory dysfunction.
XX OS Unidentified.
XX PN WO200118060-A1.
XX PD 15-MAR-2001.
XX PF 08-SEP-2000; 2000WO-JP06172.
XX PR 08-SEP-1999; 99JP-0254463.
XX PA (TORA ) TORAY IND INC.
XX PI Shimizu S, Kubota M, Akiyama H, Usui M;
XX DR WPI; 2001-290314/30.
XX PT Material for extracorporeal circulation, applicable in selective
XX PT elimination of diabetic complication factors such as carbonyl stress
XX PT products caused by abnormally promoted carbonyl stress from excretory
XX PT dysfunction in vascular lesions
XX PS Claim 1; Page 31-32; 36pp; Japanese.
XX CC The present invention describes a material for extracorporeal circulation
XX CC which is made from a water-insoluble carrier immobilized with a protein
XX CC having the sequence shown here. The materials of the invention, including
XX CC adsorbents, are for extracorporeal circulation, which are applicable in
XX CC the selective elimination of diabetic complication factors from a body
XX CC fluid, and are therefore useful in treating vascular lesions like
XX CC arteriosclerosis due to carbonyl stress products caused by abnormally
XX CC promoted carbonyl stress from excretory dysfunction.
XX SQ Sequence 404 AA;

Query Match 100.0%; Score 162; DB 22; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCCKGAPKPPORLEWK 30
   ||||||||||||||||||||||||||||
Db 23 agnitarigeplvlckgappkppqrlwkw 52

RESULT 9
AAV09350
ID AAV09350 standard; peptide: 30 AA.
XX AC AAV09350;
XX DT 09-JUL-1999 (first entry)
XX DE Mouse RAGE V-domain peptide SEQ ID NO:2.
XX RAGE: V-domain; receptor for advanced glycation endproduct;
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
XX neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
XX multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
XX tumour; cancer; male impotence; wound healing; periodontal disease;
XX neuropathy; retinopathy; nephropathy; neuronal degeneration.
XX OS Mus sp.

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XX PN WO9918987-A1.
XX PD 22-APR-1999.
XX PF 09-OCT-1998; 98WO-US21346.
XX PR 09-OCT-1997; 97US-0948131.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Lamster I, Schmidt AM, Stern D, Yan SD;
XX DR WPI; 1999-277439/23.
XX PT New peptides based on an advanced glycation end product receptor are
XX PT useful for treating Alzheimer's disease and Down's syndrome
XX PS Claim 3; Page 78; 101pp; English.
XX CC The present invention describes novel isolated peptides (1) having an
XX CC amino acid sequence corresponding to an amino acid sequence of a
XX CC V-domain of a receptor for an advanced glycation end product (RAGE).
XX CC Also described are methods for: (1) Inhibiting an amyloid-beta peptide
XX CC (ABP) interaction with a receptor for RAGE when the receptor is on the
XX CC surface of a cell; (2) Inhibiting degeneration of a neuronal cell; (3)
XX CC inhibiting formation of an ABP fibril on a cell; (4) Inhibiting
XX CC extracellular assembly of an ABP into a fibril; (5) Inhibiting
XX CC aggregation of ABP on the surface of a cell; (6) Inhibiting infiltration
XX CC of a microglial cell into senile plaques; (7) Inhibiting activation of a
XX CC macroglial cell by an ABP; (8) Treating a subject with a condition
XX CC associated with an interaction of an ABP with a receptor for RAGE on a
XX CC cell; (9) Evaluating the ability of an agent to inhibit binding of an
XX CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
XX CC Inhibiting activation of a NF-kappaB gene in a cell; (11) Inhibiting
XX CC periodontal disease in a subject; (12) Inhibiting an RAGE's interaction
XX CC with a receptor for RAGE when the receptor is on the surface of a cell;
XX CC and (13) treating a subject with a condition associated with an
XX CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
XX CC can be used for treating conditions associated with an interaction of an
XX CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
XX CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
XX CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
XX CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
XX CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
XX CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
XX CC or neuronal degeneration.
XX SQ Sequence 30 AA;

Query Match 92.0%; Score 149; DB 20; Length 30;
Best Local Similarity 93.1%; Pred. No. 1.5e-13;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTTARIGEPLVLCCKGAPKPPORLEWK 30
   |||||||||||||:|||||:||||
Db 2 qnitarigeplvlscxgappkppqglewk 30

RESULT 10
AAV09352
ID AAV09352 standard; peptide: 30 AA.
XX AC AAV09352;
XX DT 09-JUL-1999 (first entry)
XX DE Bovine RAGE V-domain peptide SEQ ID NO:4.
XX RAGE: V-domain; receptor for advanced glycation endproduct;
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;

```

KM neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KM multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KM tumour; cancer; male impotence; wound healing; periodontal disease;
 KM neuropathy; retinopathy; nephropathy; neuronal degeneration.
 OS Bos sp.
 XX WO9918987-A1.
 PN 22-APR-1999.
 PD 09-OCT-1998; 98WO-US21346.
 PF 09-OCT-1997; 97US-0948131.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX Lamster I, Schmidt AM, Stern D, Yan SD;
 PI WPI: 1999-277439/23.
 DR New peptides based on an advanced glycation end product receptor are
 XX useful for treating Alzheimer's disease and Down's syndrome
 PT Claim 5; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 XX Sequence 30 AA;

Query Match 89.5%; Score 145; DB 20; Length 30;
 Best Local Similarity 89.7%; Pred. No. 5.2e-13;
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTTARIGEPVLVKCKGAPKPPQRLWK 30
 Db 2 gntarigxplvlnckgapkppqglewk 30
 RESULT 11
 AAAY09351
 ID AAAY09351 standard; peptide; 30 AA.
 AC AAAY09351;
 XX
 DT 09-JUL-1999 (first entry)

XX Rat RAGE V-domain peptide SEQ ID NO:3.
 DE RAGE: V-domain; receptor for advanced glycation endproduct;
 XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KM senility; renal failure; hyperlipidemic atherosclerosis; dementia;
 KM neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KM multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KM tumour; cancer; male impotence; wound healing; periodontal disease;
 KM neuropathy; retinopathy; nephropathy; neuronal degeneration.
 XX Ratus sp.
 OS WO9918987-A1.
 PN 22-APR-1999.
 PD 09-OCT-1998; 98WO-US21346.
 PF 09-OCT-1997; 97US-0948131.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX Lamster I, Schmidt AM, Stern D, Yan SD;
 PI WPI: 1999-277439/23.
 DR New peptides based on an advanced glycation end product receptor are
 XX useful for treating Alzheimer's disease and Down's syndrome
 PT Claim 4; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 XX Sequence 30 AA;

Query Match 82.1%; Score 133; DB 20; Length 30;
 Best Local Similarity 82.8%; Pred. No. 2.2e-11;
 Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 QNTTARIGEPVLVKCKGAPKPPQRLWK 30
 Db 2 gntarigepvlmsckgapkppqglewk 30

RESULT 12

XX	AAW23337	
XX	AAW23337 standard; peptide; 30 AA.	
XX	AAW23337;	
XX	12-MAR-1998 (first entry)	
XX	N-terminal sequence of a protein which binds the amyloid beta peptide.	
XX	Amyloid beta peptide; extracellular deposit; Alzheimer's disease;	
XX	neurite outgrowth; microglial activation; neuronal cell degeneration;	
XX	receptor for advanced glycosylation end product;	
XX	amyloid beta peptide fibril.	
XX		
XX	Rattus sp.	
XX	WO9726913-A1.	
XX	31-JUL-1997.	
XX	21-JAN-1997; 97WO-US000857.	
XX	26-JAN-1996; 96US-0592070.	
XX	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	Schmidt AM, Stern D, Yan SD;	
XX	WPI; 1997-393374/36.	
XX	Inhibiting damage to cells in e.g. Alzheimer's disease - using an	
XX	agent which inhibits interaction of an amyloid-beta peptide with a	
XX	receptor for advanced glycosylation end product	
XX	Disclosure; Page 27; 91pp; English.	
XX		
XX	The present sequence represents the amino acid sequence of the	
XX	N-terminal of a 50 kDa cell-associated protein which binds the amyloid	
XX	beta peptide. This peptide is the principal component of extracellular	
XX	deposits in Alzheimer's disease. It has been shown to promote neurite	
XX	outgrowth, generate reactive oxygen intermediates, induce cellular	
XX	oxidant stress, lead to neuronal cytotoxicity, and promote microglial	
XX	activation. The 50 kDa protein was purified from rat epithelial cells and	
XX	is shown to be virtually identical to a bovine receptor for the advanced	
XX	glycosylation end product. Peptides derived from the amyloid beta	
XX	peptide are used in a pharmaceutical composition. This composition	
XX	comprises an agent capable of inhibiting interaction of an amyloid-beta	
XX	peptide with a receptor for advanced glycosylation end product and a	
XX	carrier. A method for inhibiting interaction of amyloid beta peptide	
XX	with a receptor for advanced glycosylation on the surface of a cell	
XX	comprises contacting the cell with e.g. present peptide. Depending on	
XX	the type of cell, inhibiting the interaction between the amyloid beta	
XX	peptide and the receptor for advanced glycosylation can be used for	
XX	inhibiting degeneration of a neuronal cell, inhibiting formation of an	
XX	amyloid beta peptide fibril on a cell, inhibiting extracellular assembly	
XX	of amyloid beta peptide into a fibril, inhibiting aggregation of amyloid	
XX	beta peptide on the surface of a cell, inhibiting infiltration of a	
XX	microglial cell into senile plaques, and inhibiting activation of	
XX	microglial cells by amyloid beta peptide. The methods can be used for	
XX	treating e.g. dementias, Alzheimer's Disease, senility, renal failure,	
XX	hyperlipidemic atherosclerosis, neuronal cytotoxicity, Down's syndrome,	
XX	dementia associated with head trauma, anisotropic lateral sclerosis,	
XX	multiple sclerosis or neuronal degeneration.	
XX	Sequence 30 AA:	

```
Query Match      78.4%; Score 127; DB 18; Length 30;
Best Local Similarity 82.8%; Pred. No. 1.5e-10;
Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

DB	2	qxitarigkplvlnxkgaapkkppqglewk	30
RESULT	13		
ID	AAW44214		
ID	AAW44214	standard; peptide: 16 AA.	
AC	AAW44214;		
XX			
DT	14-MAY-1998	(first entry)	
DE		Human soluble RAGE immunologically active fragment SHQ ID NO:18.	
XX			
XX		Human; soluble receptor; advanced glycosylation end product; RAGE;	
KW	AGE; antibody; vascular permeability; immunologically active fragment;		
KW	diabetes mellitus.		
OS	Homo sapiens.		
XX			
XX	WO9739125-A1.		
PN			
PD	23-OCT-1997.		
XX			
PF	11-APR-1997; 97WO-EP01834.		
XX			
PR	16-APR-1996; 96US-0633148.		
XX			
PA	(SCHD) SCHERING PATENTE AG.		
XX			
PI	Hollander DA, Morser MJ, Nagashima M;		
DR	WPI; 1997-558580/51.		
XX			
PT	Anti-advanced glycosylation end product polypeptide antibody -		
PT	prevents receptor binding and therefore reduces vascular		
PT	permeability, useful to treat diabetes mellitus		
XX			
PS	Claim 2; Page 49; 90pp; English.		
XX			
CC	The present sequence represents an immunologically active fragment		
CC	of a soluble human receptor to an advanced glycosylation end		
CC	product (RAGE) polypeptide. The present invention describes		
CC	an isolated antibody (Ab), specifically immunoreactive with		
CC	RAGE. Advanced glycosylation end products (AGE) of proteins are		
CC	non-enzymatically glycosylated proteins, which accumulate in vascular		
CC	tissue in ageing, and at an accelerated rate in individuals with		
CC	diabetes. The Ab, which prevents the interaction between an AGE and it's		
CC	receptor (RAGE), reduces vascular permeability. The Ab can be used to		
CC	treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive		
CC	vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis		
CC	associated amyloidosis or atherosclerosis. The Ab can also be used for		
CC	the isolation and purification of human RAGE polypeptide.		
XX			
SO	Sequence 16 AA;		
Query Match	50.0%; Score 81; DB 18; Length 16;		
Best Local Similarity	100.0%; Pred. No. 0.00015;		
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 AONTTARIGEPVLKNC 16		
DB	1 agntarigepvlknc 16		

RESULT	14
AAW33768	
ID	AAW33768 standard; peptide; 16 AA
XX	
AC	AAW33768;
XX	
DT	08-MAY-1998 (first entry)
XX	

```

DE      Human RAGE polypeptide fragment 14.
XX
KW      Advanced glycosylation end-product receptor: RAGE; screening: AGE;
KW      vascular permeability; diabetes mellitus; treatment; atherosclerosis;
XX      Alzheimer's disease.
OS      Homo sapiens.
XX
XX      MO9739121-A1.
XX
XX      23-OCT-1997.
XX
XX      11-APR-1997; 97WO-EP01832.
XX
XX      16-APR-1996; 96US-0633147.
XX
XX      (SCHD ) SCHERING AG.
XX
XX      Morser MJ, Nagashima M:
XX
XX      WPI: 1997-526458/48.
XX
XX      New soluble advanced glycosylation end-product receptor polypeptide
XX      - used for reducing vascular permeability, complications of diabetes
XX      etc., also for purification and to screen for modulators
XX
XX      Disclosure: Page 9; 91pp; English.
XX
XX      This is a peptide fragment of a human advanced glycosylation end-product
XX      receptor (RAGE) polypeptide. The RAGE polypeptides and its active
XX      fragments or their mimetics can inhibit interaction between advanced
XX      glycosylation end-products (AGE) and a receptor (specifically RAGE). They
XX      are used to treat diseases associated with AGE/RAGE interaction, such as
XX      increased vascular permeability, diabetes mellitus (particularly
XX      complications such as micro- or macro- vasculopathy or occlusive vascular
XX      disorders such as neuropathy, nephropathy, atherosclerosis or
XX      retinopathy) or haemodialysis-associated amyloidosis, also activation
XX      of microglial cells by beta-amyloid peptides in Alzheimer's disease or
XX      age-related disorders such as oxidative stress. These RAGE polypeptides
XX      are also used, when immobilised, to purify AGE from a protein mixture and
XX      to screen for compounds that are agonists and antagonists of AGE/RAGE
XX      interaction. They can also be used diagnostically to detect abnormal
XX      levels of AGE. Antibodies against RAGE polypeptides are useful as
XX      immunossay reagents for measurement of RAGE levels, and as inhibitors of
XX      interaction between AGE and RAGE or other receptors and for purification
XX      and quantification of RAGE polypeptides. The encoding nucleic acids are
XX      used to express recombinant RAGE and as probes for isolating related
XX      genes.
XX
XX      Sequence 16 AA:
XX
XX      Query Match 50.0%; Score 81; DB 18; Length 16;
XX      Best Local Similarity 100.0%; Pred. No. 0.00015;
XX      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX      QY 1 AONTARIGEPVLKC 16
XX      |||||
XX      Db 1 agntarigepvlkvc 16
XX
XX      RESULT 15
XX      ID AAM44208
XX      AAM44208 standard; peptide; 15 AA.
XX
XX      AAM44208;
XX
XX      14-MAY-1998 (first entry)
XX
XX      Human soluble RAGE immunologically active fragment SEQ ID NO:12.
XX
XX      Human; soluble receptor; advanced glycosylation end product; RAGE;
XX      AGE; antibody; vascular permeability; immunologically active fragment;
XX

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KM	diabetes mellitus.
XX	
OS	Homo sapiens.
XX	
PN	WO9739125-A1.
XX	
PD	23-0CT-1997.
XX	
PF	11-APR-1997; 97WO-EP01834.
XX	
PR	16-APR-1996; 96US-0633148.
XX	
PA	(SCHD) SCHERING PATENTE AG.
XX	
PI	Hollander DA, Morser MJ, Nagashima M;
XX	
DR	WPI; 1997-558580/51.
XX	
PT	Anti-advanced glycosylation end product polypeptide antibody -
XX	
PT	prevents receptor binding and therefore reduces vascular
XX	
PT	permeability, useful to treat diabetes mellitus
XX	
PS	Claim 2; Page 46; 90pp; English.
XX	
CC	The present sequence represents an immunologically active fragment
CC	of a soluble human receptor to an advanced glycosylation end
CC	product (RAGE) polypeptide. The present invention describes
CC	an isolated antibody (Ab), specifically immunoreactive with
CC	RAGE. Advanced glycosylation end products (AGE) of proteins are
CC	non-enzymatically glycosylated proteins, which accumulate in vascular
CC	tissue in ageing, and at an accelerated rate in individuals with
CC	diabetes. The Ab, which prevents the interaction between an AGE and it's
CC	receptor (RAGE), reduces vascular permeability. The Ab can be used to
CC	treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
CC	vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
CC	associated amyloidosis or atherosclerosis. The Ab can also be used for
CC	the isolation and purification of human RAGE polypeptide.
XX	
SO	Sequence 15 AA:
QY	Query Match 44.4%; Score 72; DB 18; Length 15;
	Best Local Similarity 100.0%; Pred. No. 0.0023;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 AQNTARIGEPYVK 15
	1 agntarigeplyvk 15
db	

Search completed: April 24, 2002, 09:17:37
Job time: 141 sec

```

Query Match          44.4%; Score 72; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0 0023;
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0.

QY      1 AONTARIGEPLVK 15
         |||
Db       1 agnltarigeplyk 15

Search completed: April 24, 2002, 09:17:37
Job time: 141 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:54 ; Search time 21.46 Seconds
(without alignments)
51.256 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 30
Sequence: 1 AONTARIGEPLVLKCKGAPKKPPQRLKWK 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	404	1	RAGE_HUMAN
2	13	43.3	403	1	RAGE_MOUSE
3	11	36.7	402	1	RAGE_RAT
4	10	33.3	416	1	RAGE_BOVIN
5	7	23.3	223	1	MUTH_HAENIN
6	7	23.3	537	1	VGIF_PVM
7	6	20.0	110	1	YG4L_YEAST
8	6	20.0	181	1	YCF4_GUTTH
9	6	20.0	210	1	YA79_HAENIN
10	6	20.0	234	1	WGP8_EBV
11	6	20.0	259	1	E434_ADECT
12	6	20.0	265	1	E434_ADECT
13	6	20.0	265	1	E434_ADECT
14	6	20.0	269	1	MIND_GUTTH
15	6	20.0	278	1	PROC_CIVBAL
16	6	20.0	282	1	MIND_CIVBAL
17	6	20.0	401	1	ENO_THREAC
18	6	20.0	429	1	RM4_CABEL
19	6	20.0	468	1	ARLY_METTH
20	6	20.0	481	1	SH2B_HUMAN
21	6	20.0	504	1	SH2B_MOUSE
22	6	20.0	513	1	SPTL_HUMAN
23	6	20.0	607	1	TVRC_PSEPL
24	6	20.0	635	1	SYT_RICPR
25	6	20.0	714	1	EFEL_MCTU
26	6	20.0	754	1	ASPH_BOVIN
27	6	20.0	757	1	ASPH_HUMAN
28	6	20.0	788	1	REC2_HAENIN
29	6	20.0	837	1	HFC2_HAENIN
30	6	20.0	837	1	HFC2_HAENIN
31	6	20.0	837	1	HFC3_HAENIN
32	6	20.0	850	1	DEXT_STRMO
33	6	20.0	879	1	YN65_YEAST

34	6	20.0	1097	1	KFLD_RAT	035787
35	6	20.0	1103	1	KFLC_HUMAN	043696
36	6	20.0	1733	1	VNDA_PVKKA	03485
37	6	20.0	2142	1	BAT2_HUMAN	04634
38	6	20.0	2210	1	RPO_TACV	020430
39	5	16.7	51	1	MLEV_MOUSE	009542
40	5	16.7	87	1	VEA_HPV51	026548
41	5	16.7	99	1	RS20_CHUPN	092712
42	5	16.7	111	1	HMG2_DROME	006943
43	5	16.7	115	1	REV_HVIMN	005871
44	5	16.7	125	1	BARW_HORVU	028814
45	5	16.7	130	1	RS9_SULAC	039468

ALIGNMENTS

RESULT 1
ID RAGE_HUMAN STANDARD: PRT: 404 AA.
AC Q15109; Q15279; Q913R3; Q9H2X7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
GN (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
GN AGER OR RAGE.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RA MEDLINE=92340547; PubMed=1378843;
RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95137587; PubMed=7835890;
RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
RA Inoko H., Ikemura T.;
RT "Three genes in the human MHC class III region near the junction with
RT products, PAX2 homeobox gene and a notch homolog, human counterpart
RT of mouse mammary tumor gene int-3.";
RL Genomics 23:408-419(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
RA Banta A., Spies T., Hood L.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.
RA Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,
RA Yamamoto H.;
RT "Molecular heterogeneity of the receptor for advanced glycation
RT endproducts.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Malherbe P., Huber G.;
RA Schuler A., Huber G.;
RT "CDNA cloning of a novel secreted isoform of the human Receptor for
RT advanced Glycation End products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant
RL amyloid precursor protein.";
RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RP [6]
RP SEQUENCE OF 1-12 FROM N.A.

RA	Hudson B.I., Futers T.S.;
RT	"Novel polymorphisms in the receptor for advanced glycation
RL	end-products (RAGE) gene."
CC	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC	-1 FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
CC	PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
CC	WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
CC	RATE IN DIABETES.
CC	-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
CC	SECRETED (ISOFORM 2).
CC	-1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/RAGESEC;
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1 TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
CC	-1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC	2 C2-LIKE AND ONE V-LIKE DOMAINS.
CC	-----
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CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M91311; AAA03574.1; -
DR	EMBL; D28769; BAA05958.1; -
DR	EMBL; U89336; AAB47491.1; -
DR	EMBL; AB036432; BAA89369.1; -
DR	EMBL; AJ133822; CAB43108.1; -
DR	EMBL; AF208289; AAC35728.1; -
DR	MIM: 600214; -
DR	InterPro: IPRO033006; IG_MHC.
DR	InterPro: IPRO033598; IG_C2.
DR	InterPro: IPRO03600; IG_Like.
DR	Pfam: PF00047; Ig; 2.
DR	SMART: SMO0408; IGC2; 1.
DR	SMART: SMO0410; IG_Like; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
KW	Alternative splicing; Polymorphism.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFD
FT	DISULFD
FT	DISULFD
FT	CARBOHYD
FT	CARBOHYD
FT	DOMAIN
FT	VARSPLIC
FT	VARSPLIC
FT	VARIANT
FT	CONFLICT
SO	SEQUENCE
Query Match	100.0%; Score 30; DB 1; Length 404;
Best Local Similarity	100.0%; Pred. No; 2,9e-25;
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	AONTARIGEPLVLCKGAPKPPQRELEWK 30

RESULT	2	
RAGE_MOUSE		
ID	RAGE_MOUSE	STANDARD; PRT: 403 AA.
AC	Q62151.	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUL-1998 (Rel. 36, Last annotation update)	
DE	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR	
DE	(RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).	
GN	AGER OR RAGE.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxId=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BALE/C; TISSUE=Lung;	
FX	MEDLINE=97368045; PubMed=9224812;	
RA	Renard C., Chappey O., Mautier M.P., Nagashima M., Lunth E.,	
RA	Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Mautier J.L.;	
RT	"Recombinant advanced glycation end product receptor pharmacokinetics	
RT	in normal and diabetic rats."	
RL	Mol. Pharmacol. 52:54-62(1997).	
CC	-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END	
CC	PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS	
CC	WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED	
CC	RATE IN DIABETES.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.	
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS	
CC	2 C2-LIKE AND ONE V-LIKE DOMAINS.	
CC	-----	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@sib-sib.ch).	
CC	-----	
DR	EMBL; L3412; AAA0040.1; .	
DR	MGD; MGI:893592; Ager.	
DR	InterPro: IPR003006; IG_MHC.	
DR	InterPro: IPR003598; IG_C2.	
DR	InterPro: IPR003600; IG_Like.	
DR	Pfam; PF00047; Ig; 3.	
DR	SMART; SM00408; IGC2; 1.	
DR	SMART; SM00410; IG_Like; 1.	
DR	PROSITE; PS00290; IG_MHC; 1.	
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.	
FT	SIGNAL	1 22
FT	CHAIN	23 403
FT	DOMAIN	23 341
FT	TRANSMEM	342 362
FT	DOMAIN	363 403
FT	DOMAIN	31 105
FT	DOMAIN	136 213
FT	DOMAIN	251 307
FT	DISULFID	38 98
FT	DISULFID	143 207
FT	DISULFID	258 300
FT	CARBOHYD	25 25
FT	CARBOHYD	80 80
FT	SEQUENCE	403 AA; 42668 MM; 1279796FD1579357 CRC64;
Query Match	43.3%;	Score 13; DB 1; Length 403;
Best Local Similarity	100.0%;	Pred. No. 7.3e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 QNTARIGEPLV 14
 |||||||||
 Db 24 QNTARIGEPLV 36

RESULT 3

RAGE_RAT
 ID RAGE_RAT STANDARD: PRT: 402 AA.

AC 063495;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;

RA MEDLINE=97368045; PubMed=9224812;

RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunth E.,

RA Morser J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;

RT "Recombinant advanced glycation end product receptor pharmacokinetics

in normal and diabetic rats.";

RL Mol. Pharmacol. 52:54-62(1997).

CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

CC RATE IN DIABETES.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.

CC -----

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CC -----

CC EMBL: U3413; AAA42027.1; -

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003600; Ig_Like.

DR Pfam: PF00047; Ig_3.

DR SMART: SM00408; IgC2.1.

DR SMART: SM00410; Ig_Like.1.

DR PROSITE: PS00290; Ig_MHC.1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 22

FT CHAIN 23 402

FT FT

FT DOMAIN 23 341

FT TRANSMEM 342 362

FT DOMAIN 363 402

FT DOMAIN 31 105

FT DOMAIN 136 212

FT DOMAIN 250 306

FT DISULFID 38 98

FT DISULFID 143 206

FT DISULFID 257 299

FT CARBOHYD 25 25

FT CARBOHYD 80 80

SO SEQUENCE 402 AA; 42663 MW; 594481BC3A51E94E CRC64;

Query Match 36.7%; Score 11; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QNTARIGEPL 12
 |||||||||
 Db 24 QNTARIGEPL 34

RESULT 4

RAGE_BOVIN
 ID RAGE_BOVIN STANDARD: PRT: 416 AA.

AC 028173;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Lung;

RA MEDLINE=92340547; PubMed=1378843;

RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,

RA Ellison K., Stern D., Shaw A.;

RT "Cloning and expression of a cell surface receptor for advanced

RT glycosylation end products of proteins.";

RL J. Biol. Chem. 267:14998-15004(1992).

CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

CC RATE IN DIABETES.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.

CC -----

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CC or send an email to license@sib-sib.ch).

CC -----

CC EMBL: M91212; AAA03575.1; -

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003600; Ig_Like.

DR Pfam: PF00047; Ig_2.

DR SMART: SM00408; IgC2.1.

DR SMART: SM00410; Ig_Like.1.

DR PROSITE: PS00290; Ig_MHC.1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 22

FT CHAIN 23 416

FT FT

FT DOMAIN 23 352

FT TRANSMEM 353 373

FT DOMAIN 374 416

FT DOMAIN 31 105

FT DOMAIN 136 213

FT DOMAIN 262 318

FT DISULFID 38 98

FT DISULFID 143 207

FT DISULFID 269 311

FT CARBOHYD 25 25

FT CARBOHYD 80 80

SO SEQUENCE 402 AA; 42663 MW; 594481BC3A51E94E CRC64;

FT DOMAIN 391 396 POLY-GLU.
SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;

Query Match 33.3%; Score 10; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKKPPQ 25
| | | | | | | | | |
DB 38 CKGAPKKPPQ 47

RESULT 5
MUTN_HAEIN.
ID MUTN_HAEIN STANDARD; PRT; 223 AA.
AC P44688;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNA MISMATCH REPAIR PROTEIN MUTN.
GN MUTN OR H10403.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; Pubmed=7542800;
RA Fleisichmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bull C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedlorn E., Cotton M.D.,
RA Ullrichback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED
GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY
SIMILARITY).
CC -----
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CC -----
CC DR EMBL; U32723; AAC22062.1; -.
DR HSSP; P06722; ZAZO.
DR TIGR; H10403; -.
KM DNA repair: Hydrolyase; Endonuclease: Complete proteome.
SQ SEQUENCE 223 AA; 24906 MW; 339A4EF9DA0E622A CRC64;

Query Match 23.3%; Score 7; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
| | | | | | | | | |
DB 165 ITARIGE 171

RESULT 6
VGLF_PVM
ID VGLF_PVM STANDARD; PRT; 537 AA.

AC P35949;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2;
DE FUSION GLYCOPROTEIN F1].
GN F.
OS Pneumonia virus of mice (PVM).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11263;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333256; Pubmed=1629698;
RA Chambers P., Pringle C.R., Easton A.J.;
RT "Sequence analysis of the gene encoding the fusion glycoprotein of
RT pneumonia virus of mice suggests possible conserved secondary
RT structure elements in paramyxovirus fusion glycoproteins.";
RL J. Gen. Virol. 73:1717-1724(1992).
CC -1- FUNCTION: THIS PROTEIN DIRECTS FUSION OF VIRAL AND CELLULAR
CC MEMBRANES, RESULTING IN VIRAL PENETRATION, & CAN DIRECT FUSION OF
CC INFECTED CELLS WITH ADJOINING CELLS, RESULTING IN THE FORMATION OF
CC SYNCYTIA.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GLYCOPROTEIN
CC FAMILY.
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CC -----
CC DR EMBL; D11128; BAA01902.1; -.
DR PIR; J01619; J01619.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 537
FT CHAIN 23 101
FT CHAIN 102 537
FT TRANSMEM 491 514
FT CARBOHYD 463 463
FT CARBOHYD 488 488
SQ SEQUENCE 537 AA; 59366 MW; BA6116E2FABE702 CRC64;
Query Match 23.3%; Score 7; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVTK 15
| | | | | | | | | |
DB 434 GEPLVTK 440

RESULT 7
YG4L_YEAST
ID YG4L_YEAST STANDARD; PRT; 110 AA.
AC P53305;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 12.4 KDA PROTEIN IN NAB1A-GP11 INTERGENIC REGION.
GN YGR215W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA MEDLINE=97435481; PubMed=9290212;
RT Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
  "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
  chromosome VII."
RL Yeast 13:1077-1090(1997).
CC -1- SIMILARITY: TO S.POMBE SPBC30D10.12C.
CC -----
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CC -----
DR EMBL: 273000; CAA97242.1; -
DR SGD: S0003447; YGR215W.
KW Hypothetical protein.
SO SEQUENCE 110 AA; 12393 MW; 05008CA4F5D09004 CRC64;

Query Match          20.0%; Score 6; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPK 22
   |||||
DB 88 KGAPK 93

RESULT 8
YCF4_GUTH
ID YCF4_GUTH STANDARD; PRT; 181 AA.
ID YCF4_67;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHOTOSYSTEM I ASSEMBLY PROTEIN YCF4.
GN YCF4.
OS Guillardia theta (Cryptomonas ph1).
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
  "The plastid genome of the cryptophyte alga, Guillardia theta:
  complete sequence and conserved syteny groups confirm its common
  ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -1- FUNCTION: SEEMS TO BE REQUIRED FOR THE ASSEMBLY OF THE PHOTOSYSTEM
CC I COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE-ASSOCIATED (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
CC -----
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CC -----
DR EMBL: AF041468; AAC35658.1; -
DR InterPro: IPR003359; Ycf4.
DR Pfam: PF02392; Ycf4; 1.
KW Photosynthesis; Thylakoid; Transmembrane; Chloroplast.
FT TRANSMEM 19 41 POTENTIAL.

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```

FT TRANSMEM 61 83 POTENTIAL.
SQ SEQUENCE 181 AA; 20921 MW; 9B74EC86AEECF48 CRC64;

Query Match          20.0%; Score 6; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RISEPL 12
   |||||
DB 153 RISEPL 158

RESULT 9
YA79_HAEIN
ID YA79_HAEIN STANDARD; PRT; 210 AA.
AC P45023;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN HI0179.
GN HI0179.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
  Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
  McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
  Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
  Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
  Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
  Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
  Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
  Venter J.C.;
  "Whole-genome random sequencing and assembly of Haemophilus
  influenzae Rd."
RL Science 269:496-512(1995).
RN [2]
RP REVISIONS.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
  Submitted (SEP-1996) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM FOR AN AMINO-ACID. PROBABLY RESPONSIBLE FOR THE
CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: U32788; AAC22735.1; -
DR TIGR: H11079; -
DR InterPro: IPR00515; BPD_transp.
DR Pfam: PF00528; BPD_transp; 1.
DR PROSITE: PS00402; BPD_TRANSF. INN MEMBR. 1.
KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
  Inner membrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.

```

FT TRANSMEM 177 197 POTENTIAL.
SQ SEQUENCE 210 AA; 23393 MW; 662C7C590DC4FDCD CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 210;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
Db 167 AONITA 172

RESULT 10
VGP8_EBV
ID VGP8_EBV STANDARD; PRT; 234 AA.
AC P03224;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE PROBABLE MEMBRANE ANTIGEN GP85.

GN EDLP3.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.

OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Segun C.,
RA Tufnell P.S., Barrett B.G.;

RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).

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CC EMBL: V01555; CA24835.1; -
DR PIR: A03787; Q0BE43.
DR PIR: S33040; S33040.
KM Membrane Glycoprotein: late protein.
SQ SEQUENCE 234 AA; 23791 MW; 48DECED0931119E CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 234;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
Db 108 AONITA 113

RESULT 11
E434_ADECT
ID E434_ADECT STANDARD; PRT; 259 AA.
AC P87568;

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EARLY E4 30 KDA PROTEIN.

OS Canine adenovirus type 2 (strain Toronto A 26-61).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=69152;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell J.B., Zhao Y.;

RT "Complete DNA sequence and genomic organization of canine
RT adenovirus type 2.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN
CC FAMILY.

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DR EMBL: U77082; AAB38735.1; -
KM Early protein.
SQ SEQUENCE 259 AA; 30014 MW; 9C966CA011C2A745 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 259;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17
Db 178 LVLKCK 183

RESULT 12
E434_ADECC
ID E434_ADECC STANDARD; PRT; 265 AA.
AC O65962;

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY E4 31 KDA PROTEIN.

OS Canine adenovirus type 1 (strain CUL).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=69150;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell J.B., Zhao Y.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE OF 248-265 FROM N.A.
RX MEDLINE=91272490; PubMed=1828920;
RA Dragulev B.P., Sira S., Abounaidar M.G., Campbell J.B.;

RT "Sequence analysis of putative E3 and fiber genomic regions of two
RT strains of canine adenovirus type 1.";

RL Virology 183:298-305(1991).
CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN
CC FAMILY.

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DR EMBL: U55001; AAB05452.1; -
KM Early protein.
SQ SEQUENCE 265 AA; 30822 MW; 92606E5E30134103 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 265;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17
Db 184 LVLKCK 189


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RESULT 13
E434_ADECR STANDARD: PRT: 265 AA.
AC 096690.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY E4 31 KDA PROTEIN.
OS Canine adenovirus type 1 (strain RI261).
OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=69151.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97275900; PubMed=9129661;
RA Morrison M.D., Onions D.E., Nicolson L.;
RL "Complete DNA sequence of canine adenovirus type 1.";
J. Gen. Virol. 78:873-878(1997).
CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 31 TO 34 KDA PROTEIN
FAMILY.
CC -----
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CC -----
DR EMBL: Y07760; CAA69046.1; -.
KM Early protein.
SQ SEQUENCE 265 AA; 30737 MW; 14B3DC9DCB1D2E15 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17
DB 184 LVLKCK 189

RESULT 14
MIND_GUTH STANDARD: PRT: 269 AA.
AC 078436.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Gullardia theta (Cryptomonas phl).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Gullardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, gullardia theta:
RT complete sequence and conserved syteny groups confirm its common
RT ancestry with red algae.";
RL J. Mol. Evol. 48:236-244(1999).
CC -1- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC -----
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CC -----
DR EMBL: D50472; BAA09063.1; -.
DR InterPro: IPR000304; P5CR.
DR Pfam: PF01089; P5CR; 1.
DR PROSITE: PS00521; P5CR; 1.
KW Oxidoreductase; Proline biosynthesis; NADP.
SQ SEQUENCE 278 AA; 29815 MW; 50359E5EF97CD68B CRC64;

Query Match 20.0%; Score 6; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
DB 35 AONITA 40

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CC -----
DR EMBL: AF041468; AAC35621.1; -.
DR InterPro: IPR000707; PARA.
DR Pfam: PF00991; PARA; 1.
KW Cell division; Septation; ATP-Binding; Chloroplast.
FT NP BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 269 AA; 29455 MW; BC363B54E689EA2 CRC64;

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Query Match 20.0%; Score 6; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVL 14
DB 215 GEPLVL 220

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RESULT 15
PROC_VIBAL STANDARD: PRT: 278 AA.
ID PROC_VIBAL
AC P52053;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
GN PROC.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=138-2;
RX MEDLINE=97137009; PubMed=8982386;
RA Nakamura T., Katoh Y., Shimizu Y., Matsuba Y., Unemoto T.;
RT "Cloning and sequencing of novel genes from Vibrio alginolyticus that
RT support the growth of K+ uptake-deficient mutant of Escherichia
RT coli.";
RL Biochim. Biophys. Acta 1277:201-208(1996).
CC -1- CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = L-PYRROLINE-5-
CC CARBOXYLATE + NAD(P)H.
CC -1- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: D50472; BAA09063.1; -.
DR InterPro: IPR000304; P5CR.
DR Pfam: PF01089; P5CR; 1.
DR PROSITE: PS00521; P5CR; 1.
KW Oxidoreductase; Proline biosynthesis; NADP.
SQ SEQUENCE 278 AA; 29815 MW; 50359E5EF97CD68B CRC64;

```

```

Query Match 20.0%; Score 6; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 AONITA 6
DB 35 AONITA 40

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Wed Apr 24 09:48:09 2002

us-09-689-469-5.oli.rsp

Page 8

Search completed: April 24, 2002, 09:24:54
Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:25 ; Search time 63.44 Seconds
(without alignments)
69.170 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 30
Sequence: 1 AONITARIGEPVLKCKGAPKPPQRLKWK 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 14627329 residues

Word size: 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	30	100.0	342	4	09Y3R3
2	13	43.3	402	11	035444
3	9	30.0	32	6	09TR01
4	7	23.3	237	5	09V5N7
5	7	23.3	330	2	09K1E6
6	7	23.3	330	2	09UX44
7	7	23.3	595	10	09LOP6
8	7	23.3	742	5	09W322
9	6	20.0	61	5	09NFI5
10	6	20.0	71	5	09N6K0
11	6	20.0	76	5	09N6T0
12	6	20.0	96	10	080389
13	6	20.0	99	10	09FR57
14	6	20.0	101	12	09JH47
15	6	20.0	127	12	09EAJ5
16	6	20.0	155	2	09SC03
17	6	20.0	209	2	006630
18	6	20.0	230	2	09RRE2
19	6	20.0	257	2	006157

20	6	20.0	259	2	09CCU3	09CCU3 mycobacteri
21	6	20.0	261	2	007711	007711 mycobacteri
22	6	20.0	271	2	067348	067348 aquifex aeo
23	6	20.0	298	2	09A7U8	09A7U8 caulobacter
24	6	20.0	298	10	09ZS04	09ZS04 arabidopsis
25	6	20.0	326	2	09HXX1	09HXX1 pseudomonas
26	6	20.0	334	5	09HXF7	09HXF7 pseudomonas
27	6	20.0	334	5	09V6W0	09V6W0 drosophila
28	6	20.0	339	11	06Z708	06Z708 rattus norv
29	6	20.0	339	11	09QYV4	09QYV4 rattus norv
30	6	20.0	359	2	088036	088036 streptomyce
31	6	20.0	359	8	09YUR6	09YUR6 protobeca
32	6	20.0	387	10	09XISO	09XISO arabidopsis
33	6	20.0	389	9	038644	038644 bacteriophage
34	6	20.0	392	2	09FCL0	09FCL0 streptomyce
35	6	20.0	411	10	09M3H9	09M3H9 cicer arict
36	6	20.0	426	5	09I7W7	09I7W7 drosophila
37	6	20.0	433	2	052912	052912 rhizobium m
38	6	20.0	452	10	09LRM5	09LRM5 arabidopsis
39	6	20.0	471	1	004928	004928 methanobact
40	6	20.0	474	2	09KSM2	09KSM2 vibrio chol
41	6	20.0	479	10	09XIT71	09XIT71 arabidopsis
42	6	20.0	479	11	09QWS2	09QWS2 mus musculu
43	6	20.0	482	4	09Y6W6	09Y6W6 homo sapien
44	6	20.0	483	11	09ESS0	09ESS0 mus musculu
45	6	20.0	483	11	09CZY9	09CZY9 mus musculu

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	342 AA.
09Y3R3	AC	09Y3R3:		
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.			
GN	RAGESEC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,			
RA	Schuler A., Huber G.;			
RT	"cDNA cloning of a novel secreted isoform of the human Receptor for			
RT	Advanced Glycation End products (RAGE) and characterization of cells			
RT	co-expressing cell-surface scavenger receptors and Swedish mutant			
RT	amyloid precursor protein."			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AJ133822; CAB43108.1; "			
DR	InterPro: IPR003598; Ig_c2.			
DR	InterPro: IPR003600; Ig_like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_2.			
DR	SMART: SM00408; IGC2; 1.			
DR	SMART: SM00410; IG_Like; 1.			
KW	SIGNAL; Receptor.			
FT	SIGNAL 1..22			POTENTIAL.
FT	CHAIN 23..342			RECEPTOR FOR ADVANCED GLYCATION END
FT				PRODUCTS.
SQ	SEQUENCE 342 AA; 36193 MW; 35DDF66A13E39B38 CRC64;			

Query Match 100.0%; Score 30; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 6e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCGAKPKPPORLEWK 30
 |||||||
 DB 23 AONTARIGEPLVLCGAKPKPPORLEWK 52

RESULT 2
 ID 035444 PRELIMINARY: PRT: 402 AA.
 AC 035444:
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE RAGE.
 GN RAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Tralcoff R., Zackrone K., Hood L.,
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF030001; AAB82007.1; -
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00408; IgC2; 1.
 DR SMART: SM00410; Ig_Like; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
 DR SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 43.3%; Score 13; DB 11; Length 402;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QONTARIGEPLVL 14
 |||||||
 DB 24 QONTARIGEPLVL 36

RESULT 3
 ID 09TR01 PRELIMINARY: PRT: 32 AA.
 AC 09TR01:
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE 35 KRA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92340546; PubMed=1321822;
 RA Schmidt A.M., Vianna M., Gerlach M., Brett J., Ryan J., Kao J.,
 RA Esposito C., Hegarty H., Hurley W., Clausen M.,
 RT "Isolation and characterization of two binding proteins for advanced
 RT glycosylation end products from bovine lung which are present on the
 RT endothelial cell surface."
 RL J. Biol. Chem. 267:14987-14997(1992).
 SO SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;

Query Match 30.0%; Score 9; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKPPQ 25
 |||||||
 DB 17 KGAPKPPQ 25

RESULT 4
 ID 09V5N7 PRELIMINARY: PRT: 237 AA.
 AC 09V5N7:
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE CG12934 PROTEIN.
 GN CG12934.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G.,
 RA Abirl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R.K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferreira S., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gottell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigbam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley J.S., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003828; AAF58764.1; -
 DR FlyBase: FBgn0033541; CG12934.
 SO SEQUENCE 237 AA; 27208 MW; C05010AD183FAF7 CRC64;

Query Match 23.3%; Score 7; DB 5; Length 237;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 KPPORLE 28
 |||||||

Db 106 KPPORLE 112

RESULT 5
 Q9KIF6 PRELIMINARY: PRT: 330 AA.

AC Q9KIF6; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C.
 GN NMB0198.

OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_Taxid=491;

Sequence from N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RA MEDLINE=20175755; PubMed=10710307;
 RT Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 Halt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Maason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 Ra Cotton M.D., Ulterback T.R., Khouri H., Qin H., Vamathevan J.,
 Ra Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
 Ra Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).

DR EMBL: AE002377; AAF40655.1; -;
 DR TIGR: NMB0198; -;
 DR InterPro: IPR000613; Pseudou_synth.
 DR InterPro: IPR002990; PSI_RLU.
 DR InterPro: IPR002942; S4;
 DR Pfam: PF00849; Pseudou_synth_2; 1.
 DR Pfam: PF01479; S4; 1.
 DR ProDom: PD001819; Pseudou_synth; 1.
 DR SMART: SM00363; S4; 1.
 DR PROSITE: PS01129; PSI_RLU; 1.
 KW Complete proteome.

Sequence 330 AA; 36682 MW; F2058C52ACE443EC CRC64;

Query Match 23.3%; Score 7; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVVK 15
 |||||
 DB 304 GEPLVVK 310

RESULT 6
 Q9JX44 PRELIMINARY: PRT: 330 AA.

AC Q9JX44; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70).
 GN RLUC OR NMA0070.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_Taxid=65699;

Sequence from N.A.
 RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
 RA MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491.";
 RL Nature 404:502-506(2000).
 DR EMBL: AL162752; CAB83386.1; -;
 DR InterPro: IPR000613; Pseudou_synth.
 DR InterPro: IPR002990; PSI_RLU.
 DR InterPro: IPR002942; S4;
 DR Pfam: PF00849; Pseudou_synth_2; 1.
 DR Pfam: PF01479; S4; 1.
 DR ProDom: PD001819; Pseudou_synth; 1.
 DR SMART: SM00363; S4; 1.
 DR PROSITE: PS01129; PSI_RLU; 1.
 KW Lyase; Complete proteome.

Sequence 330 AA; 36768 MW; 9B1AB94890F675EA CRC64;

Query Match 23.3%; Score 7; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVVK 15
 |||||
 DB 304 GEPLVVK 310

RESULT 7
 Q9LOP6 PRELIMINARY: PRT: 595 AA.

AC Q9LOP6; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE F24B9.20.
 GN F24B9.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;

Sequence from N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P.,
 RA Toriumi M., Chin C., Choi E., Chio J., Gonzalez A., Chung M.,
 RA Hwang B., Koo T., Li J., Liu A., Vaysberg M., Altati H., Brooks S.,
 RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.,
 RA Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C.,
 RA Shin P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.

Sequence from N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC007583; AAF75084.1; -;
 F5B15F9BB28B87E CRC64;

Query Match 23.3%; Score 7; DB 10; Length 595;
 Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RIGEPV 13
Db 550 RIGEPV 556

RESULT 8
Q9W322 PRELIMINARY; PRT; 742 AA.

AC Q9W322;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG3106 PROTEIN.
GN CG3106.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fiesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Maassamman D.A., Weinstein G.W., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003448; AAF46515.1; -
DR FlyBase: FBgn0030148; CG3106.
DR InterPro: IPR003862; UPF0063.
DR Pfam: PF02712; UPF0063; 1.
SQ SEQUENCE 742 AA; 84476 MW; EFF31DF7DC6DE02D CRC64;

QY 17 KGAPKP 23
Db 254 KGAPKP 260

RESULT 9
Q9NFJ5 PRELIMINARY; PRT; 61 AA.

AC Q9NFJ5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HISTONE H1.
GN H1A61.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxId=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TREU 927/4;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
DR EMBL: AJ287603; CAB76188.1; -
SQ SEQUENCE 61 AA; 6012 MW; 7B66DA10A7D33B93 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKP 22
Db 30 KGAPKP 35

RESULT 10
Q9N6K0 PRELIMINARY; PRT; 71 AA.

AC Q9N6K0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HISTONE H1.
GN H1E71 OR H1A71.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxId=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TREU 927/4;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
DR EMBL: AJ400881; CAB90839.1; -
DR EMBL: AJ287600; CAB76185.1; -
SQ SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 71;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKP 22
Db 30 KGAPKP 35

RESULT 11
Q9N6T0 PRELIMINARY; PRT; 76 AA.

AC Q9N6T0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE HISTONE H1.
 GN H1E76 OR H1E76.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxId=5702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TREU 927/4;
 RA Grueter E.;
 RL Theses (2000), Department of Parasitology, Institute of Zoology,
 RL SWITZERLAND.
 DR EMBL; AJ287605; CAB76190.1; -
 DR EMBL; AJ287601; CAB76186.1; -
 DR InterPro: IPR001386; linker_histone.
 DR PRINTS: PR00624; HISTONEH5.
 SQ SEQUENCE 76 AA; 7573 MW; 6079EF4982B50767 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 KGAPKK 22
 |||||
 DB 30 KGAPKK 35

RESULT 12
 ID 080389 PRELIMINARY; PRT; 96 AA.
 AC 080389;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CYSTEIN PROTEINASE INHIBITOR.
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxId=3659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamakawa S.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB014760; BAA28867.1; -
 DR InterPro: IPR000010; Cystatin.
 DR InterPro: IPR003243; Cystatin_C_M.
 DR Pfam: PF00031; Cystatin; 1.
 DR ProDom; PD001231; Cystatin_C_M; 1.
 DR ProSITE; PS00287; CYSTATIN; UNKNOWN_1.
 DR SMART; SM00043; CY; 1.
 SQ SEQUENCE 96 AA; 10973 MW; 027252E14B6C4F4 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 96;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17
 |||||
 DB 59 LVLKCK 64

RESULT 13
 ID 09FR57 PRELIMINARY; PRT; 99 AA.
 AC 09FR57;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)

DE SELF-PRUNING INTERACTING PROTEIN 1.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxId=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. VENT;
 RA Pnueli L., Lifschitz E.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF175963; AAG43410.1; -
 SQ SEQUENCE 99 AA; 11408 MW; E55F6975B7BA97A3 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GAPKKP 23
 |||||
 DB 45 GAPKKP 50

RESULT 14
 ID 09JH47 PRELIMINARY; PRT; 101 AA.
 AC 09JH47;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE START CODON IS NOT IDENTIFIED (FRAGMENT).
 GN E4.
 OS Human papillomavirus type 69.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxId=37121;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matsukura T., Sata T.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087389; PubMed=10618284;
 RA Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;
 RT "Molecular cloning and nucleotide sequence analysis of a novel human
 RT papillomavirus (type 82) associated with vaginal intraepithelial
 RT neoplasia."
 RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).
 DR EMBL; AB027020; BAA90731.1; -
 DR InterPro: IPR003861; Papilloma_E4.
 DR Pfam: PF02711; Pap_E4; 1.
 FT NON_TER 1
 SQ SEQUENCE 101 AA; 11267 MW; 328999BE169CAC792 CRC64;

Query Match 20.0%; Score 6; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GAPKKP 23
 |||||
 DB 39 GAPKKP 44

RESULT 15
 ID 09EAT5 PRELIMINARY; PRT; 127 AA.
 AC 09EAT5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE PROTEASE (FRAGMENT).

GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99-117635;
RA Barlow K.L., Tatt I.D., Cane P.A., Pillay D., Clewley J.P.;
RT "Detection of simple and complex recombinant strains of HIV-1 in the
UK."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
DR EMBL: AJ296662; CAC03693.1; -
DR InterPro: IPR001969; Asp_protease.
DR InterPro: IPR001995; Asp_prot-retrov.
DR Pfam: PF00077; rvp; 1.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
DR PROSITE: PS50175; ASP_PROT_RETROV; 1.
KW Aspartyl protease; Hydrolase.
FT NON_TER 1
FT NON_TER 127
SQ SEQUENCE 127 AA; 13648 MW; CEAF2745863D5F4 CRC64;

Query Match 20.0%; Score 6; DB 12; Length 127;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 ITARIG 9
| | | | |
Db 39 ITARIG 44

Search completed: April 24, 2002, 09:24:27
Job time: 251 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:01 ; Search time 38.71 Seconds
(without alignments)
59.035 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 162
Sequence: 1 AONITARIGEPLVLKCKGAPKPPORLEWK 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	404	1	I61596 advanced glycosyla
2	149	92.0	402	2	T09062 probable advanced
3	145	89.5	416	1	A42879 advanced glycosyla
4	64	39.5	3375	2	T19821 hypothetical prote
5	54	33.3	1344	2	T14316 rig-1 protein - mo
6	53.5	33.0	483	2	T17346 hypothetical prote
7	53	32.7	587	2	JH0464 DM-GRASP precursor
8	53	32.7	588	2	JH0506 adhesion molecule
9	53	32.7	588	2	A45254 surface glycoprote
10	53	32.7	602	2	A45769 acetylcholine rece
11	53	32.7	1612	2	T30805 dutil protein - mo
12	53	32.7	1651	2	T14160 transmembrane rece
13	52.5	32.4	7962	2	I38346 elastic titin - hu
14	51	31.5	757	1	S48841 secretory componen
15	51	31.5	757	1	I45956 polymeric immunogl
16	51	31.5	1260	1	S05479 neural cell adhesi
17	51	31.5	1356	2	JC1402 protein-tyrosine k
18	51	31.5	1442	2	T42607 transcription acti
19	50	30.9	284	2	D83485 probable 3-mercapt
20	50	30.9	372	2	C39371 Ig V-region-like B
21	50	30.9	386	2	A84125 hypothetical prote
22	50	30.9	392	2	A84125 acetyl-CoA acetyl
23	50	30.9	1154	2	T48829 related to SREBP c
24	50	30.9	1257	1	A41060 neural cell adhesi
25	50	30.9	1259	2	S36126 neural cell adhesi
26	50	30.9	1487	1	EDBE61 immediate-early pr
27	50	30.9	1487	1	EDBE61 155K transcrip
28	49.5	30.6	478	1	S39590 formate-dependent
29	49.5	30.6	478	2	H86100 hypothetical prote

30	49.5	30.6	1048	2	T30815	platelet-derived g
31	49	30.2	102	2	PH1238	Ig heavy chain V r
32	49	30.2	223	2	H64065	mutator muH - Hae
33	49	30.2	430	2	T28143	tapasin I homolog,
34	49	30.2	850	2	TC5700	ERB kinase activa
35	49	30.2	1239	1	A32579	neuroglian - fruit
36	49	30.2	6642	2	T29757	protein UNC-89 - C
37	48.5	29.9	438	2	C86244	DnaJ homolog, 4706
38	48.5	29.9	525	1	A58674	neurotrophin-3 rec
39	48.5	29.9	803	1	S35695	neurotrophin-3 rec
40	48.5	29.9	852	2	I51259	tyrosine kinase C
41	48.5	29.9	937	2	A45082	neurotrophic recep
42	48	29.6	337	2	B83246	probable transcrip
43	48	29.6	441	2	B70773	probable thra prot
44	48	29.6	448	2	S15018	transcription fact
45	48	29.6	508	2	A31637	transcription fact

ALIGNMENTS

RESULT 1
I61596 advanced glycosylation end-products receptor precursor - human
N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprot
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text, change 16-Jul-1999
C:Accession: I61596; B42879; S27968
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko,
Genomics 23, 408-419, 1994
A:Title: Three genes in the human MHC class III region near the junction with the cla
nterpart of mouse mammary tumor gene int-3.
A:Reference number: A55562; MIMD:95137587
A:Accession: I61596
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-404 <RES>
A:Cross-references: GB:D28769; NID:9561657; PIDN:BA05958.1; PID:9561659
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A:Reference number: A42879; MIMD:92340547
A:Accession: B42879
A:Molecule type: mRNA
A:Residues: 'G', '2-99', 'R', '101-404' <NEB>
A:Cross-references: EMBL:M91211; NID:9190845; PIDN:AAA03574.1; PID:9190846
A:Experimental source: Lung
A:Note: sequence extracted from NCBI backbone (NCBIP:109438)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
A:Gene: GDB:AGBR
A:Cross-references: GDB:306354; OMIM:600214
A:Map position: 6p21.3-6p21.3
A:Intons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT
F:23-344/Domain: extracellular #status predicted <EXT>
F:31-101/Domain: immunoglobulin homology <IM1>
F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:345-362/Domain: transmembrane #status predicted <TMW>
F:363-404/Domain: intracellular #status predicted <INT>
F:25/81/Binding site: carbonyl (Asn) (covalent) #status predicted
F:38-99,144-208,259-301/Disulfide bonds: #status predicted

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Query Match      100.0%; Score 162; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLVKCGAKPKPPQRLKWK 30
Db 23 AONTARIGEPVLVKCGAKPKPPQRLKWK 52

RESULT 2
T09062
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahern, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09062
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: EMBL:AF030001; NID:92564945; PID:92564950
A:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match      92.0%; Score 149; DB 2; Length 402;
Best Local Similarity 93.1%; Pred. No. 1.1e-13;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGEPVLVKCGAKPKPPQRLKWK 30
Db 24 QNTARIGEPVLVKCGAKPKPPQRLKWK 52

RESULT 3
A42879
advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: A42879; A42878; S27949
R:Needer, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A:Reference number: A42879; M0ID:92340547
A:Accession: A42879
A:Molecule type: mRNA
A:Residues: 1-416 <NEE>
A:Cross-references: GB:M91212; NID:9163650; PIDN:AAA03575.1; PID:9163651
A:Experimental source: Lung
A>Note: sequence extracted from NCBI backbone (NCBIP:109436)
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
R.Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A>Title: Isolation and characterization of two binding proteins for advanced glycosylati
A:Reference number: A42878; M0ID:92340546
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, 'X', 26-37, 'X', 39-49, 'XX', 52-54 <SCH>
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBIP:109434)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

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ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
A:Function:
C:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TMW>
F:373-416/Domain: intracellular #status predicted <INT>
F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match      89.5%; Score 145; DB 1; Length 416;
Best Local Similarity 89.7%; Pred. No. 4.3e-13;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGEPVLVKCGAKPKPPQRLKWK 30
Db 24 QNTARIGEPVLVKCGAKPKPPQRLKWK 52

RESULT 4
T19821
hypothetical protein ZC101.2e - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T19821; T19819; T19820; T27490; T27488; T27489; A47648; B47648;
R:Baynes, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19182
A:Accession: T19821
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3375 <WIL>
A:Cross-references: EMBL:Z93375; PIDN:CAB07569.1; GSPDB:GN00020; CESP:ZC101.2e
A:Experimental source: clone C38C6
A:Accession: T19819
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRRNAONGPLSKRTTTTTLF
A:Cross-references: EMBL:Z93375; PIDN:CAB07567.1; GSPDB:GN00020; CESP:ZC101.2a
A:Experimental source: clone C38C6
A:Accession: T19820
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1694, 'H', 1883-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRRNAON
A:Cross-references: EMBL:Z93375; PIDN:CAB07568.1; GSPDB:GN00020; CESP:ZC101.2c
R:Percy, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20375
A:Accession: T27490
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3375 <WIL>
A:Cross-references: EMBL:Z93395; PIDN:CAB07708.1; GSPDB:GN00020; CESP:ZC101.2e
A:Experimental source: clone ZC101
A:Accession: T27488
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRRNAONGPLSKRTTTTTLF
A:Cross-references: EMBL:Z93395; PIDN:CAB07706.1; GSPDB:GN00020; CESP:ZC101.2a
A:Experimental source: clone ZC101
A:Accession: T27489
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1694, 'H', 1883-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRRNAON
A:Cross-references: EMBL:Z93395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c

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A:Experimental source: clone ZC101
 A:Accession: T27487
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545,'RINVR',155
 A:Cross-references: EMBL:293335; PIDN:CA807704.1; GSPDB:GN00020; CESP:ZC101.2b
 A:Experimental source: clone ZC101
 R:Kogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
 Genes Dev. 7, 1471-1484, 1993
 A:Title: Products of the unc-52 gene in *Caenorhabditis elegans* are homologous to the coo
 A:Reference number: A47648; MID:93339574
 A:Accession: A47648
 A:Status: preliminary; nucleic acid sequence not shown
 A:Accession: T17346
 A:Molecule type: DNA
 A:Residues: 1-546,'P',548-2441,'R','KRRH',3369,'GN',3372-3373,'G',3375,'RLRHRRNAQNGPLSF
 A:Cross-references: GB:L13458
 A:Accession: B47648
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-546,'P',548-2198,'D',2290,'NAR',2294,'L',2296,'WHATE',2302-2303,'V',2305,'
 1,'ANIV',2516-2517,'L00G',2522,'IDG',2526,'S',2528,'SRGFHV',2535,'F' <R02>
 A:Cross-references: GB:L13458
 A:Accession: C47648
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-546,'P',548-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545,
 A:Cross-references: GB:L13458
 C:Genetics:
 A:Gene: CESP:ZC101.2e; CESP:ZC101.2a; CESP:ZC101.2c; CESP:ZC101.2b
 A:Map position: 2
 A:Intons: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/3
 2; 2613/1; 2684/1; 2671/1; 2813/1; 2863/1; 2900/3; 3084/1; 3176/1; 3250/2
 C:Superfamily: LDL receptor ligand-binding repeat homology; laminin-type EGF-like homolo
 C:Keywords: extracellular matrix
 F:449-183/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:190-224/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:233-268/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:955-1002/Domain: laminin-type EGF-like homology <LEG1>
 F:1011-1058/Domain: laminin-type EGF-like homology <LEG2>

Query Match 39.5%; Score 64; DB 2; Length 3375;
 Best Local Similarity 50.0%; Pred. No. 1.5;
 Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
 QY 8 IGEPLVLCCK-GAPKKPPORLEW 29
 DB 1990 VGEPLVLCCKEAFGAPGDPPEPEVM 2013
 RESULT 5
 T14316
 T19-1 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14316
 R:Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.
 submitted to the EMBL Data Library, April 1998
 A:Reference number: Z17975
 A:Accession: T14316
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1344 <YUA>
 A:Cross-references: EMBL:AF060570; NID:94206385; PID:94206386; PIDN:AAD11628.1

Query Match 33.3%; Score 54; DB 2; Length 1344;
 Best Local Similarity 32.1%; Pred. No. 16;
 Matches 9; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 3 NITARIGEPLVLCCKGAPKKPPORLEW 30
 DB 152 NNVAVAGEPVMCEVCPKGPHEPLVYTWK 179

RESULT 6
 T17346
 hypothetical protein DKFZp58601624.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17346
 R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18727
 A:Accession: T17346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-483 <DUE>
 A:Cross-references: EMBL:AL117666
 A:Experimental source: adult uterus; clone DKFZp58601624
 C:Genetics:
 A:Note: DKFZp58601624.1

Query Match 33.0%; Score 53.5; DB 2; Length 483;
 Best Local Similarity 45.5%; Pred. No. 6.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
 QY 8 IGEPLVLCCKGAPKKPPORLEW 29
 DB 96 VGEPLVLCCK-ATGNNPPRIW 116

RESULT 7
 JH0464
 DM-GRASP precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Sep-2000
 C:Accession: JH0464
 R:Burns, F.R.; von Kannen, S.; Guy, L.; Raper, J.A.; Kamholz, J.; Chang, S.
 Neuron 7, 209-220, 1991
 A:Title: DM-GRASP, a novel immunoglobulin superfamily axonal surface protein that sup
 A:Reference number: JH0464; MID:91337449
 A:Accession: JH0464
 A:Molecule type: mRNA
 A:Residues: 1-587 <BUR>
 A:Experimental source: brain
 C:Comment: This is a cell surface glycoprotein.
 C:Comment: This protein is localized to axons in the dorsal funiculus and ventral mid
 C:Keywords: glycoprotein
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-587/Product: DM-GRASP #status predicted <DMG>
 F:67,198,270,311,365,461,484,503/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 32.7%; Score 53; DB 2; Length 587;
 Best Local Similarity 40.0%; Pred. No. 9.8;
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 AONTARIGEPLVLCCKGAPKKPPQ 25
 DB 260 SOSTIKEDGNYTLCKSGNGNPPQ 284

RESULT 8
 JH0506
 adhesion molecule SCL precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
 C:Accession: JH0506; PS0270
 R:Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B
 Neuron 7, 535-545, 1991
 A:Title: Molecular cloning and expression of a novel adhesion molecule, SCL.
 A:Reference number: JH0506; MID:92030150
 A:Accession: JH0506
 A:Molecule type: mRNA

A:Residues: 1-588 <TAN>
A:Cross-references: GB:S63276; NID:g238000; PIDN:AAB20170.1; PID:g238001
A:Experimental source: embryo
A:Accession: PS0270
A:Molecule type: protein
A:Residues: 34-48 <TAN1>
C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
C:Keywords: glycoprotein; transmembrane protein
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-588/Product: adhesion molecule SC1 #status predicted <ADH>
F:500-523/Domain: transmembrane #status predicted <TRA>
F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #status predicted <BND>

Query Match 32.7%; Score 53; DB 2; Length 588;
Best Local Similarity 40.0%; Pred. No. 9.8;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCCKGAPKKRPQ 25
DB 261 SOSTIKEGDNVTLKCSGNGNPPQ 285

RESULT 9
A:Accession: A45254
surface glycoprotein BEN precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C:Accession: A45254; S19202
R:Bourguie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in
A:Reference number: A45254; MUID:92302224
A:Accession: A45254
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-588 <POU>
A:Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088
C:Keywords: glycoprotein

Query Match 32.7%; Score 53; DB 2; Length 588;
Best Local Similarity 40.0%; Pred. No. 9.8;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCCKGAPKKRPQ 25
DB 261 SOSTIKEGDNVTLKCSGNGNPPQ 285

RESULT 10
A:Accession: A45769
acetylcholine receptor synthesis stimulator ARIA-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C:Accession: A45769
R:Fallis, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.
Cell 72, 801-815, 1993
A:Title: ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of
A:Reference number: A45769; MUID:93201602
A:Accession: A45769
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-602 <FAL>
A:Cross-references: GB:L11264; NID:g212603; PIDN:AAA49037.1; PID:g212604
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIN:127787, NCBIPI:127788)
C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match 32.7%; Score 53; DB 2; Length 602;
Best Local Similarity 32.1%; Pred. No. 10;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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Oy      2 NITARIGEPLVLKCKGAPRKPPORLEW 29
       :|::|||::: | | |
Db      35 KNOEVAVGOKLVLCETTSEYPAIRFKM 62

RESULT 11
T30805
dutt1 protein - mouse
N:Alternate names: transmembrane receptor protein Robol homolog
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30805
R:M_u, M.C.; Lowe, N.; Fordham, R.; Rabbits, P.
submitted to the EMBL Data Library, July 1998
A:Description: The mouse homologue of human DUT1/H-robo1 gene: protein sequence and
A:Reference number: 220879
A:Accession: T30805
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1612 <MM>
A:Cross-references: EMBL:Y17793; NID:e1329712; PID:e1329713; PIDN:CAA76850.1
C:Genetics:
C:Gene: dutt1
A:Map position: 16

Query Match          32.7%; Score 53; DB 2; Length 1612;
Best Local Similarity 28.6%; Pred. No. 27;
Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy      3 NITARIGEPLVLKCGAKRPQRLEWK 30
       ::|||l::|: | : ||
Db     139 DVMAVAGEPAAVMCOPPRGHPEPTISMK 166

RESULT 12
T14160
transmembrane receptor protein Robol - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14160
R:kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.
Cell 92, 205-215, 1998
A>Title: Roundabout controls axon crossing of the CNS midline and defines a novel sub
A:Reference number: Z17897; MUID:98117243
A:Accession: T14160
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1651 <RID>
C:Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1
C:Function:
C:Keywords: transmembrane protein

A:Description: appears to function as the gatekeeper controlling midline crossing
```

```

Oy      2  NITARIGEPLVLKCKGAPKPPORLEW 29
      ::||::||::||::||::||::||::||
Db      35  KNOEVAVGOKLVKRCETTSEYPALEFKW 62

RESULT 11
T30805
dutt1 protein - mouse
N:Alternate names: transmembrane receptor protein Robol homolog
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30805
R:Mu, M.C.; Lowe, N.; Fordham, R.; Rabbits, P.
submitted to the EMBL Data Library, July 1998
A:Description: The mouse homologue of human DUT11/H-robol gene: protein sequence and
A:Reference number: 220879
A:Accession: T30805
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1612 <MM>
A:Cross-references: EMBL:Y17793; NID:e1329712; PID:e1329713; PIDN:CAAT6850.1
C:Experimental source: Brain
C:Genetics:
A:Gene: dutt1
A:Map position: 16

Query Match      32.7%; Score 53; DB 2; Length 1612;
Best Local Similarity 28.6%; Pred. No. 27;
Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy      3  NITARIGEPLVLKCKGAPKPPORLEWK 30
      ::|||::||::||::||::||
Db      139  DVMVAVGEPAVMECOPPRGHPEPTISWK 166

RESULT 12
T14160
transmembrane receptor protein Robol - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14160
R:Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.
Cell 92, 205-215, 1998
A:Title: Roundabout controls axon crossing of the CNS midline and defines a novel sub
A:Reference number: 217897; MUID:98117243
A:Accession: T14160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1651 <KID>
A:Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1
C:Function:
C:Keywords: transmembrane protein

A:Description: appears to function as the gatekeeper controlling midline crossing

Query Match      32.7%; Score 53; DB 2; Length 1651;
Best Local Similarity 28.6%; Pred. No. 27;
Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy      3  NITARIGEPLVLKCKGAPKPPORLEWK 30
      ::|||::||::||::||::||
Db      178  DVMVAVGEPAVMECOPPRGHPEPTISWK 205

RESULT 13
I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I38346
R:Labelt, S.; Kolmerer, B.

```

Science 270:293-296, 1995
 A:Title: titling: giant proteins in charge of muscle ultrastructure and elasticity
 A:Reference number: A57450; MUID:96026330
 A:Accession: J18346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7962 <RES>
 A:Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
 C:Genetics:
 A:Gene: GDB:TTN
 A:Cross-references: GDB:I27867; OMIM:188840
 A:Map position: 2q31-2q31

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:15 ; Search time 32.34 Seconds
(without alignments)
20.875 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 162
Sequence: 1 AONTTARIGEPVLKCKGAPKPPORLEWK 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA.*
- 2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/6CTUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	318	2	US-08-633-148-4
2	162	100.0	340	2	US-08-633-148-2
3	129	79.6	278	2	US-08-432-016-5
4	129	79.6	278	2	US-08-684-594-5
5	81	50.0	16	2	US-08-633-148-18
6	72	44.4	15	2	US-08-633-148-12
7	60	37.0	10	2	US-08-633-148-5
8	60	37.0	10	2	US-08-633-148-13
9	54	33.3	602	1	US-08-168-091A-2
10	53.5	33.0	1101	3	US-08-986-485-2
11	53	32.7	477	2	US-08-432-016-3
12	53	32.7	477	2	US-08-684-594-3
13	53	32.7	602	1	US-08-428-926-5
14	53	32.7	602	1	US-08-428-927-5
15	53	32.7	602	1	US-08-428-298-5
16	53	32.7	602	1	US-08-339-517-5
17	53	32.7	1651	4	US-09-540-245A-18
18	51	31.5	106	2	US-08-341-843B-5
19	51	31.5	106	2	US-08-427-497E-10
20	51	31.5	757	3	US-08-434-000A-6
21	51	31.5	757	4	US-09-312-157-6
22	51	31.5	767	4	US-08-874-678-2
23	51	31.5	767	3	US-08-643-839-2
24	51	31.5	788	1	US-08-232-538-15
25	51	31.5	788	2	US-08-786-164-15
26	51	31.5	1356	2	US-08-810-116-8
27	51	31.5	1356	2	US-07-930-548A-8

28	51	31.5	1356	4	US-09-098-707A-2	Sequence 2, App11
29	50	30.9	106	2	US-08-341-843B-17	Sequence 17, App1
30	50	30.9	106	2	US-08-427-497E-22	Sequence 22, App1
31	50	30.9	611	2	US-08-752-307B-10	Sequence 10, App1
32	49	30.2	388	1	US-08-429-742-4	Sequence 4, App11
33	49	30.2	407	3	US-08-753-007A-6	Sequence 6, App11
34	49	30.2	421	2	US-09-398-496-6	Sequence 1, App11
35	49	30.2	421	2	US-08-659-984A-1	Sequence 6, App11
36	49	30.2	421	4	US-08-660-531-1	Sequence 1, App11
37	49	30.2	444	2	US-08-659-984A-5	Sequence 5, App11
38	49	30.2	444	4	US-08-660-531-5	Sequence 5, App11
39	49	30.2	469	3	US-08-753-007A-8	Sequence 8, App11
40	49	30.2	469	4	US-09-398-496-8	Sequence 8, App11
41	49	30.2	615	2	US-08-752-307B-9	Sequence 9, App11
42	49	30.2	647	3	US-08-753-007A-32	Sequence 32, App1
43	49	30.2	647	4	US-09-398-496-32	Sequence 32, App1
44	48.5	29.9	601	2	US-08-795-868-16	Sequence 16, App1
45	48.5	29.9	937	2	US-08-469-537A-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-08-633-148-4
; Sequence 4, Application US/08633148
; Patent No. 5864018
GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-Apr-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: MORPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-633-148-4
Query Match 100.0%; Score 162; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AONTTARIGEPVLKCKGAPKPPORLEWK 30
|||||

Db 1 AONITARIGEPVLKCKGAPKPPQRLKWK 30

RESULT 2

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSE, MICHAEL J.

APPLICANT: MASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-2

Query Match

Best local Similarity 100.0%; Score 162; DB 2; Length 340;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGEPVLKCKGAPKPPQRLKWK 30

Db 23 AONITARIGEPVLKCKGAPKPPQRLKWK 52

RESULT 3

US-08-432-016-5

Sequence 5, Application US/08432016

Patent No. 5968768

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHYTE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,016

FILING DATE: 01-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903

FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-016-5

Query Match

Best local Similarity 79.6%; Score 129; DB 2; Length 278;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPVLKCKGAPKPPQRLKWK 30

Db 1 IGEPVLKCKGAPKPPQRLKWK 23

RESULT 4

US-08-684-594-5

Sequence 5, Application US/08684594

Patent No. 5998172

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHYTE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594

FILING DATE: 18-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016

FILING DATE: 01-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-684-594-5

Query Match 79.6%; Score 129; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLCGAPKPPORLEWK 30
|||||
DB 1 IGEPLVLCGAPKPPORLEWK 23

RESULT 5
US-08-633-148-18
Sequence 18, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-633-148-18

Query Match 50.0%; Score 81; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLC 16
|||||
DB 1 AONTARIGEPLVLC 16

RESULT 6
US-08-633-148-12
Sequence 12, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-12

Query Match 44.4%; Score 72; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLC 15
|||||
DB 1 AONTARIGEPLVLC 15

RESULT 7
US-08-633-148-5
Sequence 5, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-5

Query Match 37.0%; Score 60; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKRPQ 25
Db 1 CKGAPKKRPQ 10

RESULT 8
US-08-633-148-13
Sequence 13, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USRS THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-13

Query Match 37.0%; Score 60; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKRPQ 25
Db 1 CKGAPKKRPQ 10

RESULT 9
US-08-168-091A-2
Sequence 2, Application US/08168091A
Patent No. 5665862
GENERAL INFORMATION:
APPLICANT: Fischbach, Gerald.
APPLICANT: Falls, Douglas R.
APPLICANT: Rosen, Kenneth M.
APPLICANT: Corfas, Gabriel
TITLE OF INVENTION: Neurotrophic Factor
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE AND COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,091A
FILING DATE: 15-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,742
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: HMI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-168-091A-2

Query Match 33.3%; Score 54; DB 1; Length 602;

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,016
FILING DATE: 01-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-684-594-3

Query Match 32.7%; Score 53; DB 2; Length 477;
Best Local Similarity 40.0%; Pred. No. 8.5;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCCKGAPKPPQ 25
DB 221 SOSSTIEGDNVTLKCSGNGNPQQ 245

RESULT 13
US-08-428-926-5
Sequence 5, Application US/08428926
Patent No. 5667780
GENERAL INFORMATION:
APPLICANT: HO, Wei-Hsien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-428-926-5

Query Match 32.7%; Score 53; DB 1; Length 602;
Best Local Similarity 32.1%; Pred. No. 11;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 2 ONTARIGEPLVLCCKGAPKPPQRLW 29
DB 35 KNDVAVGOKLVLCRTTSEYPALRFKW 62

RESULT 14
US-08-428-927-5
Sequence 5, Application US/08428927
Patent No. 5756456
GENERAL INFORMATION:
APPLICANT: HO, Wei-Hsien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,927
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-428-927-5

Query Match 32.7%; Score 53; DB 1; Length 602;
Best Local Similarity 32.1%; Pred. No. 11;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 2 ONTARIGEPLVLCCKGAPKPPQRLW 29
DB 35 KNDVAVGOKLVLCRTTSEYPALRFKW 62

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RESULT 15
US-08-428-298-5
: Sequence 5, Application US/08428298
: Patent No. 5763213
: GENERAL INFORMATION:
: APPLICANT: Ho, Wei-Hsien
: APPLICANT: Osherooff, Phyllis L.
: TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: palin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/428,298
: FILING DATE: 25-APR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/339517
: FILING DATE: 14-NOV-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 853D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/952-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 602 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: US-08-428-298-5

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Search completed: April 24, 2002, 09:18:16
Job time: 175 sec

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DT 20-AUG-2001 (rel. 40, last annotation update)
 DE NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
 GN L1CAM OR CAM1 OR MIC5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031698; PubMed=1932117;
 RA Kobayashi M., Miura M., Asou H., Uyemura K.;
 RT "Molecular cloning of cell adhesion molecule L1 from human nervous
 RT tissue: a comparison of the primary sequences of L1 molecules of
 RT different origin."
 RL Biochim. Biophys. Acta 1090:238-240(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rosenthal A., Coutelle O., Drescher B.;
 RL Submitted (Apr-1994) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92329299; PubMed=1627459;
 RA Reid R.A., Hemperly J.J.;
 RT "Variants of human L1 cell adhesion molecule arise through alternate
 RT splicing of RNA."
 RL J. Mol. Neurosci. 3:127-135(1992).
 RN [4]
 RP SEQUENCE OF 353-1176 FROM N.A.
 RX MEDLINE=92020233; PubMed=1923824;
 RA Rosenthal A., Mackinnon R.N., Jones D.S.C.;
 RT "PCR walking from microdissection clone M54 identifies three exons
 RT from the human gene for the neural cell adhesion molecule L1
 RT (CAM-L1)."
 RL Nucleic Acids Res. 19:5395-5401(1991).
 RN [5]
 RP SEQUENCE OF 332-371 FROM N.A.
 RX MEDLINE=90353957; PubMed=2387585;
 RA Djafarzadeh M., Mattei M.-G., Nguyen C., Roux D., Demengeot J.,
 RA Denizot F., Moos M., Schachner M., Goridis C., Jordan B.R.;
 RT "The gene encoding L1, a neural adhesion molecule of the
 RT immunoglobulin family, is located on the X chromosome in mouse and
 RT man."
 RL Genomics 7:587-593(1990).
 RN [6]
 RP SEQUENCE OF 1030-1257 FROM N.A.
 RX MEDLINE=91132183; PubMed=1993895;
 RA Harper J.R., Prince J.T., Healy P.A., Stuart J.K., Nauman S.J.,
 RA Stallcup W.B.;
 RT "Isolation and sequence of partial cDNA clones of human L1: homology
 RT of human and rodent L1 in the cytoplasmic region."
 RL J. Neurochem. 56:797-804(1991).
 RN [7]
 RP SEQUENCE OF 20-36.
 RX MEDLINE=88298876; PubMed=3136168;
 RA Wolff J.M., Frank R., Mujoo K., Spiro R.C., Reisfeld R.A.,
 RA Ratjen F.G.;
 RT "A human brain glycoprotein related to the mouse cell adhesion
 RT molecule L1."
 RL J. Biol. Chem. 263:11943-11947(1988).
 RN [8]
 RP VARIANT HSAS TYR-264.
 RX MEDLINE=94004956; PubMed=8401576;
 RA Jouet M., Rosenthal A., Macfarlane J., Kenwrick S., Donnai D.;
 RT "A missense mutation confirms the L1 defect in X-linked hydrocephalus
 RT (HSAS)."
 RL Nat. Genet. 4:331-331(1993).
 RN [9]
 RP VARIANT HSAS/MASA LEU-1194.
 RX MEDLINE=95187172; PubMed=7681431;
 RA Fransen E., Schrander-Stumpel C., Vits L., Coucke P., van Camp G.,
 RA Willems P.J.;
 RT "X-linked hydrocephalus and MASA syndrome present in one family are
 RT due to a single missense mutation in exon 28 of the L1CAM gene."

RL Hum. Mol. Genet. 3:2255-2256(1994).
 RN [10]
 RP VARIANTS HSAS GLN-184 AND ARG-452, AND VARIANT MASA GLN-210.
 RX MEDLINE=95004608; PubMed=7920659;
 RA Jouet M., Rosenthal A., Armstrong G., Macfarlane J., Stevenson R.,
 RA Paterson J., Metzberg A., Ionescu V., Temple K., Kenwrick S.;
 RT "X-linked spastic paraplegia (SPG1), MASA syndrome and X-linked
 RT hydrocephalus result from mutations in the L1 gene."
 RL Nat. Genet. 7:402-407(1994).
 RN [11]
 RP VARIANTS MASA GLN-210 AND ASN-598.
 RX MEDLINE=95004609; PubMed=7920660;
 RA Vits L., van Camp G., Coucke P., Fransen E., de Boule K.,
 RA Reyniers E., Korn B., Poustka A., Wilson G., Schrander-Stumpel C.,
 RA Winter R.M., Schwartz C., Willems P.J.;
 RT "MASA syndrome is due to mutations in the neural cell adhesion gene
 RT L1CAM."
 RL Nat. Genet. 7:408-413(1994).
 RN [12]
 RP VARIANTS HSAS/MASA S-9; S-121; K-309; F-768; L-941 AND C-1070.
 RX MEDLINE=95282776; PubMed=7762552;
 RA Jouet M., Moncla A., Paterson J., McKeown C., Fryer A., Carpenter N.,
 RA Holmberg E., Madellus C., Kenwrick S.;
 RT "New domains of neural cell-adhesion molecule L1 implicated in
 RT X-linked hydrocephalus and MASA syndrome."
 RL Am. J. Hum. Genet. 56:1304-1314(1995).
 RN [13]
 RP VARIANTS HSAS/MASA Q-184; Q-210; Y-264; R-452; N-598 AND L-1194.
 RX MEDLINE=96153146; PubMed=8556302;
 RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;
 RT "CRASH syndrome: clinical spectrum of corpus callosum hypoplasia,
 RT retardation, adducted thumbs, spastic paraparesis and hydrocephalus
 RT due to mutations in one single gene, L1."
 RL Eur. J. Hum. Genet. 3:273-284(1995).
 RN [14]
 RP ERRATUM.
 RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;
 RL Eur. J. Hum. Genet. 4:126-126(1996).
 RN [15]
 RP VARIANTS HSAS/MASA/SPG1 SER-179 AND ARG-370.
 RX MEDLINE=96057511; PubMed=7562969;
 RA Ruiz J.C., Cuppens H., Legius E., Fryns J.-P., Glover T., Marynen P.,
 RA Cassiman J.-J.;
 RT "Mutations in L1-CAM in two families with X linked complicated
 RT spastic paraplegia, MASA syndrome, and HSAS."
 RL J. Med. Genet. 32:549-552(1995).
 RN [16]
 RP VARIANTS HSAS CYS-194 AND LEU-240.
 RX MEDLINE=97083370; PubMed=8929944;
 RA Gu S.-M., Orth U., Veske A., Enders H., Kluender K., Schloesser M.,
 RA Engel W., Schwinger E., Gal A.;
 RT "Five novel mutations in the L1CAM gene in families with X linked
 RT hydrocephalus."
 RL J. Med. Genet. 33:103-106(1996).
 RN [17]
 RP VARIANTS HSAS Q-184; V-439--T-443 DEL; C-784 AND L-936--L-948 DEL.
 RX MEDLINE=97338664; PubMed=9195224;
 RA Macfarlane J.R., Du J.-S., Peyjs M.E., Ramsden S., Donnai D.,
 RA Charlton R., Garrett C., Toimle J., Yates J.R.W., Berry C., Goudie D.,
 RA Moncla A., Lunt P., Hodgson S., Jouet M., Kenwrick S.;
 RT "Nine novel L1 CAM mutations in families with X-linked
 RT hydrocephalus."
 RL Hum. Mutat. 9:512-518(1997).
 RN [18]
 RP VARIANTS HSAS/MASA ASP-691; ARG-698 AND PRO-935.
 RX MEDLINE=98180721; PubMed=9521424;
 RA Du Y.-Z., Srivastava A.K., Schwartz C.E.;
 RT "Multiple exon screening using restriction endonuclease
 RT fingerprinting (REF) detection of six novel mutations in the L1 cell
 RT adhesion molecule (L1CAM) gene."
 RL Hum. Mutat. 11:222-230(1998).
 RN [19]
 RP VARIANT CRASH PRO-632.

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FT DOMAIN 564 649 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 681 744 IG-LIKE C2-TYPE DOMAIN 7.
FT DOMAIN 834 1162 PROTEIN KINASE.
FT NP_BIND 840 848 ATP (BY SIMILARITY).
FT BINDING 868 868 ATP (BY SIMILARITY).
FT ACT_SITE 1028 1028 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 1059 1059 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 2 2 O -> E (IN REF. 2).
FT CONFLICT 772 772 A -> T (IN REF. 3).
FT CONFLICT 787 787 R -> G (IN REF. 3).
FT CONFLICT 835 835 K -> N (IN REF. 3).
FT CONFLICT 848 848 V -> E (IN REF. 3).
FT CONFLICT 1347 1347 S -> T (IN REF. 3).
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Query Match 31.5%; Score 51; DB 1; Length 1356;
Best Local Similarity 34.5%; Pred. No. 22;
Matches 10; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

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OY 2 ONTARIGEPVLKCKGAPKPPORLEWK 30
DB 674 ENOTTSIGSEVSCIASGNPPQIMWFK 702

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RESULT 14
ID NAH2_HUMAN STANDARD; PRT; 812 AA.
AC Q9UBYO.
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SODIUM/HYDROGEN EXCHANGER 2 (NA(+)/H(+) EXCHANGER 2) (NHE-2).
GN SLC9A2 OR NHE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=99375108; PubMed=10444453;
RA Malakooti J., Dandaj R.Y., Schmidt L., Layden T.J., Dudeja P.K.,
RA Ramaswamy K.;
RT "Molecular cloning, tissue distribution, and functional expression of
RT the human Na(+)/H(+) exchanger NHE2."
RL Am. J. Physiol. 277:G383-G390(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hou S., Wohldmann P.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBS databases.
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN

```

```

CC COLONIC SODIUM ABSORPTION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND
CC KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL
CC INTESTINE.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF073299; AAD41635.1; -.
CC EMBL; AC007239; AAF19248.1; -.
CC MIM; 600530; -.
CC DR InterPro: IPR000676; NaH_Exchange.
CC DR Pfam; PF00999; Na_H_Exchange; 1.
CC DR PRINTS; PR01084; NAHEXCHNGR.
CC DR PRINTS; PR01086; NAHEXCHNGR2.
CC DR Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
CC Multigene family; Phosphorylation.
CC FT DOMAIN 1 13
CC FT DOMAIN 14 33
CC FT DOMAIN 34 79
CC FT DOMAIN 80 100
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CC FT SEQUENCE 812 AA; 91519 MW; 17EE177DC3830D0A CRC64;

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Query Match 31.2%; Score 50.5; DB 1; Length 812;
Best Local Similarity 34.4%; Pred. No. 16;
Matches 11; Conservative 4; Mismatches 6; Indels 11; Gaps 1;

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OY 10 EPLVLR-----CKGAPKPPORLEWK 30
DB 765 QPLLSKDGSGSEREDSLTEGIPKPPRLWVR 796

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RESULT 15
ID CAML_HUMAN STANDARD; PRT; 1257 AA.
AC P32004;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

FT	DOMAIN	440	503	IG-LIKE C2-TYPE DOMAIN 5.
FT	DOMAIN	531	599	IG-LIKE C2-TYPE DOMAIN 6.
FT	DOMAIN	827	896	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	932	994	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	1032	1094	FIBRONECTIN TYPE-III 3.
FT	SITE	553	555	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	562	564	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	504	504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	587	587	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	725	725	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	776	776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	824	824	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	848	848	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	875	875	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	968	968	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	978	978	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1030	1030	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1073	1073	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1183	1183	MISSING (IN SHORT ISOFORM) (BY SIMILARITY).
SO	SEQUENCE	1260 AA;	140968 MM;	22BE57001CB2A538 CRC64;

Query Match	31.5%;	Score 51;	DB 1;	Length 1260;
Best Local Similarity	42.9%;	Pred. No. 21;		
Matches	9;	Conservative	2;	Mismatches 10; Indels 0; Gaps 0;

Oy	9	GEPLVLCCKGAPKRPQRLW	29
Db	150	GESVVLPCNPSPSAAPRIYW	170

RESULT	13			
ID	VGR2_HUMAN	STANDARD:	PRT:	1356 AA.
AC	P35968;	O60723;	Q14178;	
DT	01-JUN-1994	(Rel. 29, Created)		
DT	20-AUG-2001	(Rel. 40, Last sequence update)		
DT	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112)			
DE	(VEGFR-2) (KINASE INSERT DOMAIN RECEPTOR) (FLK-1).			
GN	KDR OR FLK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yin L.Y., Wu Y., Patterson C.;			
RT	"Full length human KDR/Flk-1 sequence.";			
RL	Submitted (Dec-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=umbilical vein;			
RA	Yu Y., Whitney R.G., Sato J.D.;			
RT	"Coding region for human VEGF receptor KDR (VEGFR-2).";			
RL	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 3-1356 FROM N.A.			
RC	TISSUE=umbilical vein;			
RX	MEDLINE=92019839; PubMed=1655671;			
RA	Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L., Shows T.B.;			

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RT      "Identification of a new endothelial cell growth factor receptor
RL      tyrosine kinase."
RN      Oncogene 6:1677-1683(1991).
RN      [4]
RX      SEQUENCE OF 1-22 FROM N.A.
RX      MEDLINE=96032749; PubMed=7559454;
RA      Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,
RA      Harder E.;
RT      "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT      receptor for vascular endothelial growth factor."
RL      J. Biol. Chem. 270:23111-23118(1995).
RN      [5]
RP      FUNCTION
RX      MEDLINE=93038639; PubMed=1417831;
RX      Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
RA      Armellino D.C., Gospodarowicz D., Boehlen P.;
RT      "Identification of the KDR tyrosine kinase as a receptor for vascular
RT      endothelial cell growth factor."
RL      Biochem. Biophys. Res. Commun. 187:1579-1586(1992).
CC      -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC      KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC      PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC      VASCULAR PERMEABILITY.
CC      -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE ~ ADP + PROTEIN
CC      TYROSINE PHOSPHATE
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC      PROTEIN KINASES.
CC      -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL, AF035121; AAB88005.1; -
DR      EMBL, AF063658; AAC16450.1; -
DR      EMBL, X61656; CAA43837.1; -
DR      EMBL, L04947; AAA56459.1; -
DR      EMBL, X89776; CAA61916.1; -
DR      HSSP, P11362; IAGW.
DR      MIM, 191306; -
DR      InterPro: IPR000719; Euk_pkinase.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003598; Ig_C2.
DR      InterPro: IPR003600; Ig_Like.
DR      InterPro: IPR01824; Rptor_tyr_kin_III.
DR      InterPro: IPR01245; Tyr_kin.
DR      Pfam: PF00047; Ig_6.
DR      Pfam: PF00069; pkinase_2.
DR      SMART, SM00408; IGC2_2.
DR      SMART, SM00410; IG_Like; 4.
DR      SMART, SM00219; TyKc; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR      PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW      Signal, transferase, tyrosine-protein kinase; Receptor; Transmembrane;
KW      Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
FT      SIGNAL 1 19
FT      CHAIN 20 1356
FT      VASCULAR ENDOTHELIAL GROWTH FACTOR
FT      RECEPTOR 2.
FT      DOMAIN 20 764
FT      TRANSMEM 765 789
FT      TRANSMEM 790 1356
FT      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN 46 110
FT      IG-LIKE C2-TYPE DOMAIN 1.
FT      DOMAIN 141 207
FT      IG-LIKE C2-TYPE DOMAIN 2.
FT      DOMAIN 239 314
FT      IG-LIKE C2-TYPE DOMAIN 3.
FT      DOMAIN 345 400
FT      IG-LIKE C2-TYPE DOMAIN 4.
FT      DOMAIN 438 537
FT      IG-LIKE C2-TYPE DOMAIN 5.

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CC TISSUE-Mammary gland;
 RX MEDLINE-96069604; PubMed-7590352;
 RA Verbeet M.P., Vermeer H., Warner G.C., de Boer H.A., Lee S.H.;
 RT "Cloning and characterization of the bovine polymeric immunoglobulin
 RT receptor-encoding cDNA."
 RL Gene 164:329-333(1995).
 CC -1- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
 CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
 CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
 CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
 CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
 CC TRANSMEMBRANE SEGMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS (A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: FOUND IN MAMMARY GLAND, JEJUNUM, LUNG,
 CC KIDNEY AND SMALL INTESTINE.
 CC -1- PTM: IN THE ABSENCE OF DIMERIC IGA, SER-727 IS PHOSPHORYLATED
 CC WHICH ALLOWS PIGR TO FUNCTION NORMALLY.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L04797; AAC41620.1; -;
 DR EMBL: X81371; CAA57136.1; -;
 DR InterPro: IPR003599; Ig_1;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_5;
 DR SMART: SM00409; Ig_4;
 DR SMART: SM00410; Ig_Like; 1.
 DR Immunoglobulin domain: Repeat; Transmembrane; Glycoprotein; Signal;
 KW Polymorphism: Phosphorylation: Alternative splicing.
 FT SIGNAL 1 18
 FT CHAIN 19 757
 FT CHAIN 19 599
 FT DOMAIN 19 632
 FT TRANSMEM 633 653
 FT DOMAIN 654 757
 FT DOMAIN 19 132
 FT DOMAIN 133 238
 FT DOMAIN 239 350
 FT DOMAIN 351 462
 FT DOMAIN 463 575
 FT DISULFID 403 110
 FT DISULFID 56 64
 FT DISULFID 152 220
 FT DISULFID 257 324
 FT DISULFID 271 279
 FT DISULFID 370 440
 FT DISULFID 384 394
 FT DISULFID 481 543
 FT DISULFID 485 519
 FT DISULFID 495 502
 FT CARBOHYD 83 83
 FT CARBOHYD 420 420
 FT CARBOHYD 468 468
 FT MOD_RES 727 727
 FT VARSPPLIC 129 346
 FT VARIANT 29 29
 FT VARIANT 142 142
 FT VARIANT 144 404
 FT VARIANT 413 413
 FT VARIANT 435 435
 SQ SEQUENCE 757 AA: 82434 MW: DCEDE67FDD6A656C6 CRC64;

Query Match 31.5%; Score 51; DB 1; Length 757;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 QNTTARGEPLVLK 16
 Db 467 KNTYAWLGEPLKLS 481
 :1:1:111111
 RESULT 12
 CAML_MOUSE
 ID CAML_MOUSE STANDARD; PRT; 1260 AA.
 AC P11627;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
 GN NCAM OR CAML.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-Brain;
 RX MEDLINE-88318924; PubMed-3412448;
 RA Moos M., Tacke R., Scherer H., Teplov D., Fruh K., Schachner M.;
 RT "Neural adhesion molecule L1 as a member of the immunoglobulin
 RT superfamily with binding domains similar to fibronectin."
 RL Nature 334:701-703(1988).
 CC -1- FUNCTION: CELL ADHESION MOLECULE WITH AN IMPORTANT ROLE IN THE
 CC DEVELOPMENT OF THE NERVOUS SYSTEM. INVOLVED IN NEURON-NEURON
 CC ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS
 CC TO AXONIN ON NEURONS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS IN THE CYTOPLASMIC REGION ARE
 CC PRODUCED BY DIFFERENTIAL SPLICING (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X12875; CAA31368.1; -;
 DR PIR: S05479; S05479.
 DR HSSP: P20241; 1CFA.
 DR MGD: MGI:96721; L1cam
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00041; fn3; 4.
 DR Pfam: PF00047; Ig_6.
 DR PRINTS: PR00014; FNTYPEIII.
 DR SMART: SM00406; FN3; 3.
 DR SMART: SM00408; IgC2; 5.
 DR SMART: SM00410; Ig_Like; 1.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
 KW Immunoglobulin domain; Signal; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 1260
 FT DOMAIN 20 1123
 FT TRANSMEM 1124 1146
 FT DOMAIN 1147 1260
 FT DOMAIN 50 120
 FT DOMAIN 150 215
 FT DOMAIN 256 318
 FT DOMAIN 346 410
 NEURAL CELL ADHESION MOLECULE L1.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE DOMAIN 1.
 IG-LIKE C2-TYPE DOMAIN 2.
 IG-LIKE C2-TYPE DOMAIN 3.
 IG-LIKE C2-TYPE DOMAIN 4.

DB 36 QVVTAVEYQAILACKTPKKTSSRLKMW 64

RESULT 10

NRG1_XENIA STANDARD: PRT; 677 AA.

ID NRG1_XENIA 093383; Q9W6N0.

AC 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DR 20-AUG-2001 (Rel. 40, Last annotation update)

DE PRO-NEUREGULIN-1 PRECURSOR (PRO-NRG1) [CONTAINS: NEUREGULIN-1].

GN NRG1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8335;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM ALPHA1), AND ALTERNATIVE SPLICING.

RX MEDLINE=98352126; PubMed=9685585;

RA Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., Tsim K.W.K.;

RT Cloning of cDNAs encoding xenopus neurotrophin expression in myotomal muscle during embryo development.

RL Brain Res. Mol. Brain Res. 58:59-73(1998).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM CRD).

RX MEDLINE=99316087; PubMed=10383827;

RA Yang J.F., Zhou H., Choi R.C., Ip N.Y., Peng H.B., Tsim K.W.K.;

RT A cysteine-rich form of Xenopus neurotrophin induces the expression of acetylcholine receptors in cultured myotubes.

RL Mol. Cell. Neurosci. 13:415-429(1999).

CC -1- FUNCTION: DIRECT LIGAND FOR THE ERBB TYROSINE KINASE RECEPTORS. INDICES EXPRESSION OF ACETYLCHOLINE RECEPTOR IN SYNAPTIC NUCLEI.

CC -1- SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: ALPHA1 (SHOWN HERE) AND CRD/CRD-NRG1 (CYSTEINE RICH DOMAIN); ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS HAVE ALPHA OR BETA-TYPE EGF-LIKE DOMAINS.

CC -1- TISSUE SPECIFICITY: ISOFORM ALPHA1 IS EXPRESSED IN BRAIN AND MUSCLE. ISOFORM CRD IS EXPRESSED IN BRAIN AND SPINAL CORD, BUT AT VERY LOW LEVEL IN MUSCLE.

CC -1- DEVELOPMENTAL STAGE: STRONG EXPRESSION IN DEVELOPING BRAIN AND SPINAL CORD OF THE EMBRYO. ALSO EXPRESSED IN THE MYOTOMAL MUSCLE.

CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).

CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN.

CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM.

CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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CC EMBL: AF076618; AAC26804.1; -

DR EMBL: AF142632; AAD33893.1; -

DR HSSP: 002297; IHRF.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR002154; Neuregulin.

DR Pfam: PF00008; EGF. 1.

DR Pfam: PF00047; Ig. 1.

DR Pfam: PF02158; Neuregulin. 1.

DR PRINTS: PR01089; NEUREGULIN.

DR SMART: SM00181; EGF. 1.

DR SMART: SM00408; IGC2. 1.

DR PROSITE: PS00023; EGF. 1.

DR PROSITE: PS0186; EGF. 2; 1.

KW Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein; Transmembrane; Alternative splicing.

FT CHAIN 1 259

FT CHAIN 1 677

FT DOMAIN 1 260

FT TRANSMEM 261 280

FT DOMAIN 281 677

FT DOMAIN 50 119

FT DOMAIN 188 232

FT DISULFID 57 116

FT DISULFID 192 206

FT DISULFID 200 220

FT DISULFID 222 231

FT DOMAIN 1 25

FT CARBOHYD 124 124

FT CARBOHYD 130 130

FT VARSPIC 1 136

FT VARSPIC 223 252

FT VARSPIC 677 AA; 75794 MW; 49279E8F5BAE396F CRC64;

SO SEQUENCE

Query Match 31.5%; Score 51; DB 1; Length 677;

Best Local Similarity 38.1%; Pred. No. 11;

Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 9 GEPVLKCKGAPKPPORLEW 29

Db 50 GKILVKQAVSEDSLKFRW 70

RESULT 11

ID PIGR_BOVIN STANDARD: PRT; 757 AA.

AC P81265;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DR 20-AUG-2001 (Rel. 40, Last annotation update)

DE POLYMERIC-IMMUNOGLOBULIN RECEPTOR PRECURSOR (POLY-IG RECEPTOR) (PIGR) [CONTAINS: SECRETORY COMPONENT].

GN PIGR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN (1)

RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

RC TISSUE=Small intestine, and Mammary gland;

RX MEDLINE=95186063; PubMed=7880445;

RA Kulseth M.A., Krajaei P., Myklebost O., Rogne S.;

RT Cloning and characterization of two forms of bovine polymeric immunoglobulin receptor cDNA.

RL DNA Cell Biol. 14:251-256(1995).

RN (2)

RP SEQUENCE FROM N.A.

CC		EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM.
CC	-1-	PYM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).
CC	-1-	SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC	-1-	SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-1-	SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC		-----
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CC		-----
DR	EMBL:	L11264; AAA49037.1; .
DR	EMBL:	AF045654; AAC05670.1; .
DR	EMBL:	AF045655; AAC05671.1; .
DR	EMBL:	AF045656; AAC05672.1; .
DR	HSSP:	O02297; IHRE.
DR	InterPro:	IPR000561; EGF-like.
DR	InterPro:	IPR003006; Ig_MHC.
DR	InterPro:	IPR003598; Ig_C2.
DR	InterPro:	IPR002154; Neuregulin.
DR	Pfam:	PF00047; Ig; 1.
DR	Pfam:	PF02158; Neuregulin; 1.
DR	PRINTS:	PR01089; NEUREGULIN.
DR	SMART:	SM00181; EGF; 1.
DR	SMART:	SM00408; IGC2; 1.
DR	PROSITE:	PS00022; EGF_1; 1.
DR	PROSITE:	PS01186; EGF_2; FALSE NEG.
KW	Growth factor;	EGF-like domain; Immunoglobulin domain; glycoprotein;
KW	Transmembrane;	Alternative splicing.
FT	CHAIN	1 602 PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM.
FT	CHAIN	1 205 NEUREGULIN-1.
FT	DOMAIN	1 206 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	207 229 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT	DOMAIN	230 602 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	42 112 IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	125 136 SER/THR-RICH.
FT	DOMAIN	137 181 EGF-LIKE.
FT	DISULFID	49 105 BY SIMILARITY.
FT	DISULFID	141 155 BY SIMILARITY.
FT	DISULFID	149 169 BY SIMILARITY.
FT	CARBOHYD	171 180 BY SIMILARITY.
FT	CARBOHYD	21 21 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	113 113 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	126 126 N-LINKED (GLCNAC...) (POTENTIAL).
FT	VARSPLIC	1 127 MMATSEGGLOYSLATPDVNSYNTVPKLRKKNOEVAY GKRVLCETTSVEPALRFKLKGKGTETTKNRENKIKPK KKKYSELHTRATLADNGERACVSKSLGDSTKSAVIIT DTNA -> MSVEGETEFPSPSAQLSPASISGLAEENMPG PHRDSRPVGVAGLASTCVCCLAEERKGLCINSERICIAP LACLISLICLAGLKAEVDKIFEYDSPHTLPGRIODDP STVDPALSAWPEVVAASPPRIPSLSKAETVQTOSSIV SPREFLOSLYNRLIDVGMSAPSPLSSPLEPTYSOAO ATERNLOTAPKLS (IN ISOFORM BETA1, ISOFORM BETA2A AND ISOFORM BETA2B). MISSING (IN ISOFORM BETA2A AND ISOFORM BETA2B).
FT	VARSPLIC	191 198 VSAMTTTPARMSPVDFHP -> HTPPTSLLACKVSLRVS (IN ISOFORM BETA2B).
FT	VARSPLIC	388 405 MISSING (IN ISOFORM BETA2B).
FT	VARSPLIC	406 602 MISSING (IN ISOFORM BETA2B).
SO	SEQUENCE	602 AA: 67453 MW: 4183CDE5CED3d46 CRC64;

Query Match	32.7%	Score 53	DB 1	Length 602
Best Local Similarity	32.1%	Pred. NO. 5.2		
Matches	9	Conservative	7	Matches 12; Indels 0; Gaps 0;
QY	2	ONITARIGEPVLKCKGAKKPPQRL	EW 29	
	:1	:1:111:1:	:1111:	

DB	35	KN6EVAVGQKLVLRCEETSEYPAIRFKM	62
RESULT	9		
ID	VEJA_HUMAN	STANDARD:	PRT: 298 AA.
AC	P57087		
DT	20-AUG-2001 (Rel. 40, Created)		
DT	20-AUG-2001 (Rel. 40, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JAM).		
GN	C21ORF43.		
OC	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Vascular endothelial cells;		
RX	Medline:20317114; PubMed:10779521;		
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;		
RT	"Vascular endothelial junction-associated molecule, a novel member of		
RT	the immunoglobulin superfamily, is localized to intercellular		
RT	boundaries of endothelial cells.";		
RL	J. Biol. Chem. 275:19139-19145(2000).		
CC	-1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO		
CC	SECONDARY LYMPHOID ORGANS.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).		
CC	-1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL		
CC	VEICLES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.		
CC	LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL		
CC	CELLS.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.		
CC	-----		
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CC	-----		
DR	EMBL: AF255910; AAF81223.1; -		
DR	InterPro: IPR0033006; IG_MMC.		
DR	InterPro: IPR003398; IG_C2.		
DR	InterPro: IPR003600; IG_Like.		
DR	Pfam: PF00047; Ig; 2.		
DR	SMART: SMO0408; IGC2; 1.		
DR	SMART: SMO0410; IG_Like; 1.		
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	298
FT	DOMAIN	21	238
FT	TRANSMEM	239	259
FT	DOMAIN	260	298
FT	DOMAIN	43	116
FT	DOMAIN	148	221
FT	DISULFID	50	109
FT	DISULFID	155	214
FT	CARBOHYD	98	98
FT	CARBOHYD	187	187
FT	CARBOHYD	236	236
FT	SEQUENCE	298 AA;	33207 MM;

Query Match 32.1%, Score 52; DB 1; Length 296;
Best Local Similarity 41.4%; Pred. No. 3.6;
Matches 12; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

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RX MEDLINE=92302224; PubMed=16089332.
RA Pourquie O., Cordon C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT "BEN", a surface glycoprotein of the immunoglobulin superfamily, is
RL expressed in a variety of developing systems";
RN Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RP [4]
RZ POSSIBLE FUNCTION.
RX MEDLINE=92211411; PubMed=1313497;
RA Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RT "Association of BEN glycoprotein expression with climbing fiber
RL axonogenesis in the avian cerebellum.";
RN J. Neurosci. 12:1548-1557(1992).
CC -I- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC FIBER AXONOGEMESIS. SUPPORTS NEURITE EXTENSION.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC EPITHELIAL, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC OF BEN.
CC -I- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC DEVELOPMENT.
CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC 3 C2-LIKE AND 2 V-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: S63276; AAB20170.1; -.
DR EMBL: M76678; AAA48602.1; -.
DR EMBL: X64301; CAA45579.1; -.
DR HSSP: Q13740; IKDC.
DR InterPro: IPRO03599; IG.
DR InterPro: IPRO03006; IG_MHC.
DR InterPro: IPRO03600; IG_1like.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00409; IG_3.
DR SMART: SM00410; IG_1like; 2.
DR ProSITE: PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL. 1 33
FT CHAIN. 34 588
FT DOMAIN. 34 532 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM. 533 553 POTENTIAL.
FT DOMAIN. 554 588 CYTOPLASMIC (POTENTIAL).
FT DOMAIN. 42^ 126 IG-LIKE V-TYPE DOMAIN 1.
FT DOMAIN. 156 233 IG-LIKE V-TYPE DOMAIN 2.
FT DOMAIN. 269 326 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN. 352 404 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN. 433 497 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFD. 49 119 POTENTIAL.
FT DISULFD. 163 226 POTENTIAL.
FT DISULFD. 276 319 POTENTIAL.
FT DISULFD. 359 397 POTENTIAL.
FT DISULFD. 440 490 POTENTIAL.
FT CARBOHD. 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 485 485 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHD. 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT. 2 10 MEPPAAR->EPPSRRP (IN REF. 3).
FT CONFLICT. 25 25 A->S (IN REF. 3).

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FT CONFLICT 112 113 SD -> R (IN REF. 3).
FT CONFLICT 329 329 A -> T (IN REF. 2).
FT CONFLICT 401 402 LQ -> HK (IN REF. 2).
SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match 32.7%; Score 53; DB 1; Length 588;
Best Local Similarity 40.0%; Pred. No. 5.1;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AON1ARIGEPLVTKCKGAPKKPPQ 25
Db 261 SOSSTIKESDNYTLKCSGNGNPPQ 285

RESULT 8
NRG1_CHICK
ID NRG1_CHICK STANDARD. PRT; 602 AA.
AC 005199; 073750; 073751; 073752;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-1 PRECURSOR (PRO-NRG1) [CONTAINS: NEUREGULIN-1
DE (ACETYLCHOLINE RECEPTOR INDUCING ACTIVITY) (ARIA)].
GN NRG1 OR ARIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM ARIA), AND PARTIAL SEQUENCE.
RC STRAIN=WHITE LECHORN; TISSUE=Brain;
RX MEDLINE=93201602; PubMed=8453670;
RA Falls D.L., Rosen K.M., Corfas G., Iane W.S., Fischbach G.D.;
RT "ARIA, a protein that stimulates acetylcholine receptor synthesis, is
RT a member of the neu ligand family.";
RL Cell 72:801-815(1993).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS BETA1A; BETA2A AND BETA2B).
RC TISSUE=Brain, and Spinal cord;
RX MEDLINE=98150951; PubMed=9491987;
RA Yang X., Kuo Y., Devay P., Yu C., Role L.;
RT "A cysteine-rich isoform of neuregulin controls the level of
RT expression of neuronal nicotinic receptor channels during
RT synaptogenesis.";
RL Neuron 20:255-270(1998).
CC -1- FUNCTION: DIRECT LIGAND FOR THE ERBB TYROSINE KINASE RECEPTORS.
CC THE MULTIPLE ISOFORMS PERFORM DIVERSE FUNCTIONS: CYSTEINE-RICH
CC DOMAIN CONTAINING ISOFORMS (CRD-NRG) PROBABLY REGULATE THE
CC EXPRESSION OF NICOTINIC ACETYLCHOLINE RECEPTORS AT DEVELOPING
CC INTERNEURONAL SYNAPSES. THE IG-NRG ISOFORM IS REQUIRED FOR THE
CC INITIAL INDUCTION AND/OR MAINTENANCE OF THE MATURE LEVELS OF
CC ACETYLCHOLINE RECEPTORS AT NEUROMUSCULAR SYNAPSES.
CC -1- SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A
CC PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-
CC BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: ARIA/IG-NRG (SHOWN
CC HERE), CRD-NRG-BETA1A, CRD-NRG-BETA2A AND CRD-NRG-BETA2B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. ARIA CONTAINS AN IG-LIKE DOMAIN,
CC WHEREAS IN THE CRD-NRG (OR NARIA) ISOFORMS, THE EGF-LIKE DOMAIN IS
CC REPLACED BY A CYSTEINE-RICH DOMAIN (CRD).
CC -1- DEVELOPMENTAL STAGE: CRD-NRG ISOFORM IS DETECTED AT EMBRYONIC DAY
CC 4 (Ed4) IN BOTH VISCERAL AND SOMATIC MOTOR NEURONS OF SPINAL CORD
CC AND IS HIGHEST AT ED6. IG-NRG ISOFORM IS NOT EXPRESSED UNTIL ED 6
CC IN SPINAL CORD. AT ED 11 BOTH ISOFORMS DISPLAY COMPARABLE LEVELS.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY)
CC -1- DOMAIN: ENBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN.
CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE

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FT DISULFID 1718 1766 BY SIMILARITY.
 FT DISULFID 1813 1860 BY SIMILARITY.
 FT DISULFID 1906 1953 BY SIMILARITY.
 FT DISULFID 1997 2052 BY SIMILARITY.
 FT DISULFID 2098 2146 BY SIMILARITY.
 FT DISULFID 2194 2241 BY SIMILARITY.
 FT DISULFID 2283 2328 BY SIMILARITY.
 FT DISULFID 2373 2419 BY SIMILARITY.
 FT CARBOHYD 1421 1421 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 2481 AA; 270812 MW; E47FBE2B310F5031 CRC64;

Query Match 39.5%; Score 64; DB 1; Length 2481;
 Best Local Similarity 50.0%; Pred. No. 0.59;
 Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

OY 8 IGEPLVKCK--GAPKKPQRLPM 29
 Db 1989 VGEPLVKCEAFGAPGDPPEVEM 2012

RESULT 6
 FVB_MOUSE STANDARD; PRT; 819 AA.
 AC 035601; 0992H3;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FYN-BINDING PROTEIN (FYN-T-BINDING PROTEIN) (FVB-120/130) (P120/P130)
 DE (SLP-76 ASSOCIATED PHOSPHOPROTEIN) (SLAP-130).
 GN FVB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FVB-120).
 RC TISSUE=T-cell lymphoma;
 RX MEDLINE=97352826; PubMed=9207119;
 RA da Silva A.J., Li Z., de Vera C., Canto E., Findell P., Rudd C.E.;
 RT "Cloning of a novel T-cell protein FVB that binds FYN and SH2 domain-
 RT containing leukocyte protein 76 and modulates Interleukin 2
 RT production.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:7493-7498(1997).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM FVB-130).
 RC TISSUE=Hybridoma;
 RX MEDLINE=99428514; PubMed=10497204;
 RA Veale M., Raab M., Li Z., da Silva A.J., Kraeft S.-K., Wieremowicz S.,
 RA Morton C.C., Rudd C.E.;
 RT "Novel isoform of lymphoid adaptor FYN-T-binding protein (FVB-130)
 RT interacts with SLP-76 and up-regulates Interleukin 2 production.";
 RT J. Biol. Chem. 274:28427-28435(1999).
 RL [2]
 CC -1- FUNCTION: ACTS AS A ADAPTER PROTEIN OF THE FYN AND SH2-DOMAIN-
 CC CONTAINING LEUCOCYTE PROTEIN-76 (SLP76) SIGNALING CASCADES IN T
 CC CELLS. MODULATES THE EXPRESSION OF INTERLEUKIN-2 (IL-2).
 CC -1- SUBUNIT: INTERACTS WITH FYN AND SLP76.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, FVB-130 (SHOWN HERE) AND FVB-
 CC 120. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEMATOPOIETIC TISSUES SUCH AS
 CC MYELOID AND T CELLS, SPLEEN AND THYMUS. NOT EXPRESSED IN B CELLS,
 CC NOR IN NON-LYMPHOID TISSUES. FVB-130 IS PREFERENTIALLY EXPRESSED
 CC IN MATURE T-CELLS COMPARED TO FVB-120. WHEREAS THYMOCYTES SHOWED A
 CC GREATER RELATIVE AMOUNT OF FVB-120.
 CC -1- PTM: T-CELL RECEPTOR LIGATION LEADS TO INCREASED TYROSINE
 CC PHOSPHORYLATION.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL: AF001863; AAB62227.1; -
 DR EMBL: AF061744; AAD03267.1; -
 DR WGD; MG1:1346327; Fyb.
 DR InterPro: IPR002965; P_R1ch_extensn.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR01217; PRICEXTENS.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW SH3 domain; Phosphorylation; Nuclear protein; Coiled coil;
 KW Alternative splicing.
 FT DOMAIN 343 348 POLY-PRO.
 FT DOMAIN 381 385 POLY-PRO.
 FT DOMAIN 448 495 COILED COIL (POTENTIAL).
 FT DOMAIN 479 493 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 584 587 SH2-BINDING (TO SLP-76).
 FT DOMAIN 606 609 POLY-PRO.
 FT DOMAIN 615 618 SH2-BINDING (TO FYN).
 FT DOMAIN 622 625 POLY-ASP.
 FT DOMAIN 696 699 POLY-PRO.
 FT DOMAIN 699 756 SH3.
 FT DOMAIN 710 736 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 739 805 SH3-LIKE.
 FT VARSPLIC 627 672 MISSING (IN ISOFORM FVB-120).
 SQ SEQUENCE 819 AA; 90055 MW; 6222C7EF1CA2BBD CRC64;

Query Match 34.6%; Score 56; DB 1; Length 819;
 Best Local Similarity 44.4%; Pred. No. 2.6;
 Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

OY 1 AQNTARIGEPVLV--KCKGAPKKRPQ 25
 Db 213 SKNPVOKGSPVQAKSKGAPFKRPK 239

RESULT 7
 C166_CHICK STANDARD; PRT; 588 AA.
 ID C166_CHICK
 AC P42292;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE C0166 ANTIGEN PRECURSOR (SCI GLYCOPROTEIN) (BEN GLYCOPROTEIN) (DM-
 DE GRASP PROTEIN) (JC7 PROTEIN).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
 RC TISSUE=Embryo.
 RX MEDLINE=92030150; PubMed=1931049;
 RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
 RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
 RT "Molecular cloning and expression of a novel adhesion molecule, SCI-2,"
 RL Neuron 7:535-545(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91337449; PubMed=1873027;
 RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
 RA Chang S.;
 RT "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
 RT that supports neurite extension.";
 RL Neuron 7:209-220(1991).
 RL [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
 RC TISSUE=Bursa of fabricius;


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FT CARBOHYD 80 80 N-LINKED (GLICAC- ) (POTENTIAL).
SQ SEQUENCE 402 AA; 42663 MW; 554401BCCA51E94E CRC64;

Query Match 85.8%; Score 139; DB 1; Length 402;
Best Local Similarity 86.2%; Pred. No. 2,4e-12;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 QNITARIGEPVLTKCKGAPKPPQLEWK 30
DB 24 QNITARIGEPVLTKCKGAPKPPQLEWK 52

RESULT 5
UN52_CAEEL
ID UN52_CAEEL STANDARD: PRT; 2401 AA.
AC Q06561;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DR BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).
GN UNC-52.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93339574; PubMed=893416;
RA Rogalski T.M., Williams B.D., Mullen G.P., Moerman D.G.;
RT "Products of the unc-52 gene in Caenorhabditis elegans are homologous
RT to the core protein of the mammalian basement membrane heparan
RT sulfate proteoglycan.";
RL Genes Dev. 7:1471-1484(1993).
CC -! FUNCTION: PROBABLE ROLE IN MYOFILAMENT ASSEMBLY AND/OR ATTACHMENT
CC OF THE MYOFILAMENT LATTICE TO THE CELL MEMBRANE. UNC-52 MAY BE AN
CC EXTRACELLULAR ANCHOR FOR INTEGRIN RECEPTORS IN MUSCLE.
CC -! SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -! ALTERNATIVE PRODUCTS: UNC-52 PRODUCES AT LEAST THREE POLYPEPTIDES:
CC ONE VERY SHORT FORM AND TWO LONG FORMS.
CC -! TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANE OF ALL
CC CONTRACTILE TISSUES. IT IS CONCENTRATED OVER MUSCLE DENSE BODIES.
CC AND M-LINES WHICH ARE ASSOCIATED WITH BETA-INTEGRIN.
CC -! DEVELOPMENTAL STAGE: SYNTHESIZED EARLY IN EMBRYOGENESIS.
CC -! SIMILARITY: CONTAINS 3 LDL-RECEPTOR CLASS A DOMAINS.
CC -! SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -! SIMILARITY: CONTAINS 7 LAMININ EGF-LIKE DOMAINS.
CC -! SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -----
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CC -----
CC EMBL; L13458; AAA28156.1; -.
DR HSSP; P01130; IAJJ.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003598; Iq_C2.
DR InterPro; IPR003600; Iq_Like.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR000519; P_trefoil.
DR Pfam; PF00047; Iq; 16.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00053; laminin_EGF; 5.
DR Pfam; PF00057; IqL_recept_A; 3.
DR ProDom; PD003031; Laminin_B; 2.

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DR	SMART: SM00180; EGF_Lam; 5.	FT	SIGNAL	1	18	POSTENITAL.
DR	SMART: SM00408; ICG2; 11.	FT	CHAIN	19	2481	BASEMENT MEMBRANE PROTEGLICYCAN.
DR	SMART: SM00410; IG-like; 5.	FT	DOMAIN	19	148	IG-LIKE C2-TYPE DOMAIN 1.
DR	SMART: SM00281; Lamb; 2.	FT	DOMAIN	149	188	LDL-RECEPTOR CLASS A 1.
DR	SMART: SM00192; Ldla; 3.	FT	DOMAIN	190	229	LDL-RECEPTOR CLASS A 2.
DR	SMART: SM00018; P; 1.	FT	DOMAIN	233	272	LDL-RECEPTOR CLASS A 3.
DR	PROSITE: PS00022; EGF_1; 4.	FT	DOMAIN	273	363	IG-LIKE C2-TYPE DOMAIN 2.
DR	PROSITE: PS01029; LDLRA_1; 3.	FT	DOMAIN	384	431	LAMININ EGF-LIKE 1 (INCOMPLETE)
DR	PROSITE: PS50068; LDLRA_2; 3.	FT	DOMAIN	432	441	LAMININ EGF-LIKE 2 (N-TERMINAL)
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	442	632	LAMININ DOMAIN IV 1.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	633	665	LAMININ EGF-LIKE 1.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	673	719	LAMININ EGF-LIKE 2 (C-TERMINAL)
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	720	729	LAMININ EGF-LIKE 3 (INCOMPLETE)
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	730	920	LAMININ EGF-LIKE 4 (N-TERMINAL)
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	921	953	LAMININ DOMAIN IV 2.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	934	1003	LAMININ EGF-LIKE 4 (C-TERMINAL)
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1010	1059	LAMININ EGF-LIKE 5.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1060	1110	LAMININ EGF-LIKE 6.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1133	1216	LAMININ EGF-LIKE 7.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1227	1311	IG-LIKE C2-TYPE DOMAIN 3.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1318	1403	IG-LIKE C2-TYPE DOMAIN 4.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1415	1499	IG-LIKE C2-TYPE DOMAIN 5.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1507	1592	IG-LIKE C2-TYPE DOMAIN 6.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1598	1682	IG-LIKE C2-TYPE DOMAIN 7.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1699	1785	IG-LIKE C2-TYPE DOMAIN 8.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1785	1878	IG-LIKE C2-TYPE DOMAIN 9.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1887	1976	IG-LIKE C2-TYPE DOMAIN 10.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1977	2070	IG-LIKE C2-TYPE DOMAIN 11.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	2078	2162	IG-LIKE C2-TYPE DOMAIN 12.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	2174	2260	IG-LIKE C2-TYPE DOMAIN 13.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	2267	2347	IG-LIKE C2-TYPE DOMAIN 14.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	2354	2436	IG-LIKE C2-TYPE DOMAIN 15.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	66	114	IG-LIKE C2-TYPE DOMAIN 16.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	149	161	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	156	174	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	168	183	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	190	202	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	197	215	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	209	224	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	233	246	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	240	259	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	253	268	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	954	963	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	956	970	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	973	982	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	985	1001	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1010	1020	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1012	1026	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1029	1038	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1041	1057	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1060	1078	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1062	1081	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1081	1090	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1093	1108	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.	FT	DOMAIN	1151	1199	BY SIMILARITY.
DR	PROSITE: PS01026; LDLRA_1; 3.					

Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGEPVLKCKGAPKPPQLEWK 30
 |||||
 DB 24 QNTARIGEPVLKCKGAPKPPQLEWK 52

RESULT 3
 RAGE_BOVIN STANDARD; PRT; 416 AA.

AC 028173;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92340547; PubMed=1378843;
 RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
 RA Elliston K., Stern D., Shaw A.;
 RT "Cloning and expression of a cell surface receptor for advanced
 RT glycosylation end products of proteins."
 RT J Biol Chem. 267:14998-15004(1992).
 RL J Biol Chem. 267:14998-15004(1992).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M91212; AAA03575.1; -
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003598; Ig_C2.
 CC InterPro: IPR003600; Ig_Like.
 CC Pfam: PF00047; Ig2.
 CC SMART: SM00408; IgC2.1.
 CC SMART: SM00410; Ig_Like; 1.
 CC PROSITE: PS00290; Ig_MHC; 1.
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 416
 FT DOMAIN 23 352
 FT TRANSMEM 353 373
 FT DOMAIN 374 416
 FT DOMAIN 31 105
 FT DOMAIN 136 213
 FT DOMAIN 262 318
 FT DISULFID 38 98
 FT DISULFID 143 207
 FT DISULFID 269 311
 FT CARBOHYD 25 25
 FT CARBOHYD 80 80
 FT DOMAIN 391 396
 FT SEQUENCE 416 AA; 44182 MW; B70381573E767AE CRC64;

Query Match 89.5%; Score 145; DB 1; Length 416;
 Best Local Similarity 89.7%; Pred: No. 3.5e-13;
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGEPVLKCKGAPKPPQLEWK 30
 |||||
 DB 24 QNTARIGEPVLKCKGAPKPPQLEWK 52

RESULT 4
 RAGE_RAT STANDARD; PRT; 402 AA.

AC 063495;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunn E.,
 RA Morser J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RT in normal and diabetic rats."
 RT Mol. Pharmacol. 52:54-62(1997).
 RL M01. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L33413; AAA42027.1; -
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003598; Ig_C2.
 CC InterPro: IPR003600; Ig_Like.
 CC Pfam: PF00047; Ig2.3.
 CC SMART: SM00408; IgC2.1.
 CC SMART: SM00410; Ig_Like; 1.
 CC PROSITE: PS00290; Ig_MHC; 1.
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 402
 FT DOMAIN 23 341
 FT TRANSMEM 342 362
 FT DOMAIN 363 402
 FT DOMAIN 31 105
 FT DOMAIN 136 212
 FT DOMAIN 250 306
 FT DISULFID 38 98
 FT DISULFID 143 206
 FT DISULFID 257 299
 FT CARBOHYD 25 25
 FT SEQUENCE 402 AA; 44182 MW; B70381573E767AE CRC64;

RA Hudson B.I., Futers T.S.;
 RT "Novel polymorphisms in the receptor for advanced glycation
 end-products (RAGE) gene."
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 CC - FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
 CC SECRETED (ISOFORM 2).
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/RAGESEC;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC - TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: M91211; AAA03574.1; -
 CC EMBL: D28769; BAA05958.1; -
 CC EMBL: U89336; BAA47491.1; -
 CC EMBL: AB036432; BAA89369.1; -
 CC EMBL: AJ133822; CAB43108.1; -
 CC EMBL: AF208289; AAG35728.1; -
 CC MIM: 600214; -
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR InterPro: IPR003598; Ig_C2.
 CC DR Pfam: PF00047; Ig_2.
 CC DR SMART: SM00408; IgC2; 1.
 CC DR SMART: SM00410; Ig_Like; 1.
 CC DR ProSITE: PS00290; Ig_MHC; 1.
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
 CC Alternative splicing; Polymorphism.
 CC FT SIGNAL 1 22 POTENTIAL.
 CC FT CHAIN 23 404 ADVANCED GLYCOSYLATION END PRODUCT-
 CC SPECIFIC RECEPTOR.
 CC FT DOMAIN 23 342 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 343 363 POTENTIAL.
 CC FT DOMAIN 364 404 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 31 106 IG-LIKE V-TYPE DOMAIN.
 CC FT DOMAIN 137 214 IG-LIKE C2-TYPE DOMAIN 1.
 CC FT DOMAIN 252 308 IG-LIKE C2-TYPE DOMAIN 2.
 CC FT DISULFID 38 99 POTENTIAL.
 CC FT DISULFID 144 208 POTENTIAL.
 CC FT DISULFID 259 301 POTENTIAL.
 CC FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT DOMAIN 380 384 POLY-GU.
 CC FT VARSPLIC 54 67 MISSING (IN ISOFORM 2).
 CC FT VARSPLIC 275 404 GVPLPLPSPVLILPEIGPODQSYSCVATSHSGPOESRA
 CC VISITIEPEEGPTAGSGGLTALALGILGGLTAL
 CC LIGVILMORRORGERKAPENDEEEERAEALNOSPEPAG
 CC ESTGTGP -> VSDERAGRTIRGGANRCLGRIRAGNS
 CC PGPGDGRPGDSRPAHWGHLVAAATPRGEEGPRPGGNG
 CC GACRTESVGT (IN ISOFORM 2).
 CC Q -> R.
 CC /FTID-VAR.011338.
 CC M -> G (IN REF. 1).
 CC CONFLICT 1 1
 CC SEQUENCE 404 AA; 42802 MW; 0D584C436C30CE7 CRC64;

Query Match 100.0%; Score 162; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLVKCKGAPKRPORLEWK 30

DB 23 AONTARIGEPVLVKCKGAPKRPORLEWK 52
 RESULT 2
 RAGE_MOUSE
 ID RAGE_MOUSE STANDARD; PRT; 403 AA.
 AC 062151;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Mautier M.P., Nagashima M., Lunn E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherzmann J.M., Mautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 in normal and diabetic rats."
 RL Mol. Pharmacol. 52:54-62(1997).
 CC - FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L33412; AAA00040.1; -
 CC MGD: MGI:893592; Ager.
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR InterPro: IPR003598; Ig_C2.
 CC DR InterPro: IPR003600; Ig_Like.
 CC DR Pfam: PF00047; Ig_3.
 CC DR SMART: SM00408; IgC2; 1.
 CC DR SMART: SM00410; Ig_Like; 1.
 CC DR ProSITE: PS00290; Ig_MHC; 1.
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 CC FT SIGNAL 1 22 POTENTIAL.
 CC FT CHAIN 23 403 ADVANCED GLYCOSYLATION END PRODUCT-
 CC SPECIFIC RECEPTOR.
 CC FT DOMAIN 23 341 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 342 362 POTENTIAL.
 CC FT DOMAIN 363 403 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 31 105 IG-LIKE V-TYPE DOMAIN.
 CC FT DOMAIN 136 213 IG-LIKE C2-TYPE DOMAIN 1.
 CC FT DOMAIN 251 307 IG-LIKE C2-TYPE DOMAIN 2.
 CC FT DISULFID 38 98 POTENTIAL.
 CC FT DISULFID 143 207 POTENTIAL.
 CC FT DISULFID 258 300 POTENTIAL.
 CC FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 403 AA; 42668 MW; 1279796F5D1579357 CRC64;

Query Match 92.0%; Score 149; DB 1; Length 403;
 Best Local Similarity 93.1%; Pred. No. 9.1e-14;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:39 ; Search time 21.42 Seconds

(without alignments)
51.351 Million cell updates/sec

Title: US-09-689-469-5

Perfect score: 162

Sequence: 1 AONTATIGEPVLKCKGAPKPPQLEWK 30

ALIGNMENTS

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description	
1	162	100.0	404	1	RAGE_HUMAN	015109 homo sapien
2	149	92.0	403	1	RAGE_MOUSE	062151 mus musculu
3	145	86.5	416	1	RAGE_BOVIN	028173 bos taurus
4	139	85.8	402	1	RAGE_RAT	063495 ratus norv
5	64	39.5	2481	1	UN52_CAEEL	006561 caenorhabd
6	34.6	819	1	FVB_MOUSE	035601 mus musculu	
7	35	32.7	588	1	C166_CHICK	P42922 gallus gall
8	53	32.7	602	1	NR61_CHICK	005199 gallus gall
9	52	32.1	298	1	VEJA_HUMAN	P57087 homo sapien
9	51	31.5	677	1	NR61_XENLA	093383 xenopus lae
10	51	31.5	757	1	PIGR_BOVIN	P11627 mus musculu
11	51	31.5	1260	1	CAML_MOUSE	P35968 homo sapien
12	51	31.5	1356	1	VGR2_HUMAN	090490 homo sapien
13	51	31.5	1356	1	CAML_MOUSE	P32004 homo sapien
14	50.5	31.2	812	1	NAH2_HUMAN	005695 ratus norv
15	50	30.9	1257	1	CAML_HUMAN	P28925 equine herp
16	50	30.9	1259	1	CAML_RAT	P17473 equine herp
17	50	30.9	1487	1	ICP4_HSVB	P32050 escherichia
18	50	30.9	1487	1	ICP4_HSVB	094939 ratus norv
19	49.5	30.6	478	1	NRPA_ECOLI	P44688 haemophilus
20	49.5	30.6	922	1	NR61_RAT	073895 gallus gall
21	49	30.2	223	1	MUTH_XAEIN	014511 homo sapien
22	49	30.2	430	1	TPSN_CHICK	014511 homo sapien
23	49	30.2	850	1	NR62_HUMAN	091044 gallus gall
24	49	30.2	1302	1	NR62_HUMAN	001973 homo sapien
25	48.5	29.9	827	1	TRKC_CHICK	092139 mus musculu
26	48.5	29.9	937	1	ROR1_HUMAN	075662 homo sapien
27	48.5	29.9	937	1	ROR1_MOUSE	090718 gallus gall
128	48.5	29.9	3038	1	TRIO_HUMAN	010601 mycobacteri
129	48	29.6	375	1	SRE_CHICK	P23790 xenopus lae
30	48	29.6	441	1	DHOM_MYCTU	P11831 homo sapien
31	48	29.6	448	1	SRE_XENLA	P56974 mus musculu
32	48	29.6	508	1	SRE_HUMAN	
33	48	29.6	756	1	NR62_MOUSE	

34	48	29.6	811 1 FS22_DROME	P34083 drosophila
35	48	29.6	868 1 NR62_RAT	035569 ratus norv
36	48	29.6	873 1 FS21_DROME	P34082 drosophila
37	47.5	29.3	837 1 NCW2_MOUSE	035136 mus musculu
38	47.5	29.3	923 1 NR61_MOUSE	P97333 mus musculu
39	47.5	29.3	943 1 ROR2_HUMAN	001974 homo sapien
40	47.5	29.3	944 1 ROR2_MOUSE	092138 mus musculu
41	47.5	29.3	953 1 LYAG_MOUSE	P70699 mus musculu
42	47.5	29.3	1147 1 KMLS_RABIT	P29294 oryctolagus
43	47	29.0	400 1 HHP2_SCHPO	P40236 schizosacch
44	47	29.0	985 1 REVI_YEAST	P12689 saccharomyc
45	46.5	28.7	326 1 UL10_HCVVA	P16843 human cytom

RESULT 1	STANDARD:	PRT:	404 AA.
ID	RAGE_HUMAN		
AC	015109: 015279: 09Y3R3: 09H2X7:		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR		
DE	(RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).		
GN	AGER OR RAGE.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Lung:		
RX	MEDLINE=92340547; PubMed=1378843;		
RA	Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,		
RA	Elliston K., Stern D., Shaw A.;		
RT	"Cloning and expression of a cell surface receptor for advanced		
RT	glycosylation end products of proteins."		
RL	J. Biol. Chem. 267:14998-15004(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RX	MEDLINE=95137587; PubMed=7835890;		
RA	Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,		
RA	Inoko H., Ikemura T.;		
RT	"Three genes in the human MHC class III region near the junction with		
RT	the class II: gene for receptor of advanced glycosylation end		
RT	products, PBX2 homeobox gene and a notch homolog, human counterpart		
RL	of mouse mammary tumor gene int-3.";		
RL	Genomics 23:408-419(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RA	Rosen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,		
RA	Banta A., Spies T., Hood L.;		
RT	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.		
RA	Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,		
RA	Yamamoto H.;		
RT	"Molecular heterogeneity of the receptor for advanced glycation		
RT	endproducts."		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORM 2)		
RA	Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,		
RA	Schuler A., Huber G.;		
RT	"CDNA cloning of a novel secreted isoform of the human Receptor for		
RT	advanced glycation end products (RAGE) and characterization of cells		
RT	co-expressing cell-surface scavenger receptors and Swedish mutant		
RT	amyloid precursor protein."		
RL	Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	SEQUENCE OF 1-12 FROM N.A.		

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:11 ; Search time 62.94 Seconds
(without alignments)
69.720 Million cell updates/sec

Title: US-09-689-469-5
Perfect score: 162
Sequence: 1 AONTARIGEPVLKCKGAPKPPQRLKWK 30

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTEMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	342	4	09Y3R3
2	149	92.0	402	11	035444
3	108	66.7	32	6	09TR01
4	64	39.5	2295	5	09XRD2
5	64	39.5	2482	5	018263
6	64	39.5	3375	5	09XRT5
7	63	38.9	1482	5	09V4Y0
8	61	37.7	2016	5	09V4J9
9	61	37.7	2016	5	09NBA1
10	58	35.8	1215	5	09V787
11	56.5	34.9	1791	5	09NSC2
12	55.5	34.3	1496	4	092626
13	55	34.0	848	5	025198
14	54	33.3	1344	11	09Z214
15	53.5	33.0	483	4	09UR14
16	53	33.0	1094	4	09BYB8
17	53	32.7	762	5	09U2E2
18	53	32.7	886	5	09VM64
19	53	32.7	1612	11	089026

20	53	32.7	1651	4	09Y6N7	09Y6N7 homo sapien
21	53	32.7	1651	11	055005	055005 rattus norv
22	52.5	32.4	7962	4	010465	010465 homo sapien
23	52	32.1	99	10	09FR57	09FR57 lycopersico
24	52	32.1	181	11	09CMD9	09CMD9 mus musculu
25	52	32.1	298	11	09J159	09J159 mus musculu
26	52	32.1	1793	5	09NKJ4	09NKJ4 leishmania
27	51	31.5	305	7	098261	098261 homo sapien
28	51	31.5	455	4	09UR0	09UR0 homo sapien
29	51	31.5	1442	12	042066	042066 equine heip
30	50.5	31.2	212	10	09FGP8	09FGP8 arabidopsis
31	50.5	31.2	793	11	070246	070246 mus musculu
32	50.5	31.2	1114	4	09BWL1	09BWL1 homo sapien
33	50	30.9	284	2	09I452	09I452 pseudomonas
34	50	30.9	372	7	031406	031406 gallus galli
35	50	30.9	377	5	09VHR0	09VHR0 drosophila
36	50	30.9	386	10	004645	004645 arabidopsis
37	50	30.9	392	2	09K6C8	09K6C8 bacillus ha
38	50	30.9	538	11	09OX07	09OX07 mus musculu
39	50	30.9	1154	3	09PM63	09PM63 neurospora
40	50	30.9	1234	11	09R044	09R044 rattus norv
41	50	30.9	1252	11	09QXK7	09QXK7 rattus norv
42	50	30.9	1252	11	09J1X2	09J1X2 rattus norv
43	50	30.9	1259	11	09QY38	09QY38 mus musculu
44	49.5	30.6	921	11	09OX38	09OX38 rattus norv
45	49.5	30.6	968	5	09VCM6	09VCM6 drosophila

ALIGNMENTS

RESULT 1
ID 09Y3R3 PRELIMINARY; PRT; 342 AA.
AC 09Y3R3;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
GN RA6SEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Matherbe P., Richards J., Gaillard H., Thompson A., Diener C.,
RA Schuler A., Huber G.;
RT "CDNA cloning of a novel secreted isoform of the human Receptor for
RT Advanced Glycation End products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant
RT amyloid precursor protein.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC 1-SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AJ133822; CAB43108.1; -
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IgC2; 1.
DR SMART: SM00410; Ig_Like; 1.
KW Signal; Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 342 RECEPTOR FOR ADVANCED GLYCATION END
FT PRODUCTS.
SQ SEQUENCE 342 AA; 36193 MW; 35DDF66A13E39B38 CRC64;

Query Match 100.0%; Score 162; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 5.1e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKKPPORLEWK 30
 DB 23 AONTARIGEPVLKCKGAPKKPPORLEWK 52

RESULT 2
 ID 035444 PRELIMINARY; PRT: 402 AA.
 AC 035444;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JUN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE RAGE.
 GN RAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;
 RL Submitted (JCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF030001; AAB82007.1; -
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00408; IgC2; 1.
 DR SMART: SM00410; Ig_like; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 92.0%; Score 149; DB 11; Length 402;
 Best Local Similarity 93.1%; Pred. No. 5.1e-14;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30
 DB 24 ONTARIGEPVLKCKGAPKKPPORLEWK 52

RESULT 3
 ID 09TR01 PRELIMINARY; PRT: 32 AA.
 AC 09TR01;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE 35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92340546; PubMed=1321822;
 RA Schmidt A.M., Viana M., Gerlach M., Brett J., Ryan J., Kao J.,
 RA Esposito C., Hegarty H., Hurley W., Clauss M.;
 RT "Isolation and characterization of two binding proteins for advanced
 RT glycosylation end products from bovine lung which are present on the
 RT endothelial cell surface."
 RL J. Biol. Chem. 267:14987-14997(1992).
 SQ SEQUENCE 32 AA; 3507 MW; AEA43147CE5B3D91 CRC64;

Query Match 66.7%; Score 108; DB 6; Length 32;
 Best Local Similarity 75.9%; Pred. No. 4.7e-09;
 Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30
 DB 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30

RESULT 4
 ID 09XTD2 PRELIMINARY; PRT: 2295 AA.
 AC 09XTD2;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE UNC-52 PROTEIN.
 GN UNC-52 OR ZC101.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RA Percy C., Baynes C.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A (O18263),
 CC ISOFORM ZC101.2B (O18261), ISOFORM ZC101.2C (SHOWN HERE) AND
 CC ISOFORM ZC101.2E (O9XTD15); MAY BE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
 CC (LDLR) DOMAIN.
 DR EMBL: Z93395; CAB07707.1; -
 DR EMBL: Z93375; CAB07568.1; JOINED.
 DR EMBL: Z93395; CAB07568.1; JOINED.
 DR HSSP: P01130; ILDR.
 DR WormPep: ZC101.2C; CE15034.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR002172; LDL_recept_A.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR000519; P_trefoll.
 DR Pfam: PF00047; Ig; 14.
 DR Pfam: PF00052; Laminin_B; 2.
 DR Pfam: PF00053; Laminin_EGF; 5.
 DR Pfam: PF00057; Idl_recept_a; 3.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR PRODOM: PD003031; Laminin_B; 2.
 DR SMART: SM00180; EGF_Lam; 5.
 DR SMART: SM00408; IgC2; 9.
 DR SMART: SM00410; Ig_like; 5.
 DR SMART: SM00281; Lamb; 2.
 DR SMART: SM00192; LDLa; 3.
 DR SMART: SM00182; P; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_4.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
 DR PROSITE: PS01209; LDLR_1; 3.
 DR PROSITE: PS00068; LDLR_2; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
 KW Alternative splicing: EGF-like domain; Glycoprotein;
 KW Hypothetical protein: Laminin EGF-like domain; Repeat.
 SQ SEQUENCE 2295 AA; 251087 MW; F6BC6067ABF86C48 CRC64;

Query Match 39.5%; Score 64; DB 5; Length 2295;
 Best Local Similarity 50.0%; Pred. No. 1.2;

Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
QY 8 IGEPLVKCK--GAPKKPQRLFM 29
Db 1803 VGEPLQVKEAFGAPGDPPEVEM 1826)

RESULT 5
ID 018263 PRELIMINARY; PRT: 2482 AA.
AC 018263;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
UN 01-NOV-2001 (TrEMBLrel. 17, last annotation update)
GN UNC-52 OR ZC101.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Percy C., Baynes C.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS: ISOFORM ZC101.2A (SHOWN HERE),
CC ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (09XTD2) AND ISOFORM
CC ZC101.2E (09XT15); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
CC (LDLRA) DOMAIN.
DR EMBL: Z93395; CAB07706.1; JOINED.
DR EMBL: Z93375; CAB07569.1; JOINED.
DR EMBL: Z93395; CAB07569.1; JOINED.
DR HSSP: P01130; ILDR.
DR WormRep: ZC101.2A; CE15028.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR000519; P_trefoll.
DR Pfam: PF00047; Ig_16.
DR Pfam: PF00052; Laminin_B_2.
DR Pfam: PF00053; Laminin_EGF_5.
DR Pfam: PF00057; Idl_recept_a; 3.
DR ProDom: PD003031; Laminin_B_2.
DR SMART: SM00180; EGF_Lam; 5.
DR SMART: SM00408; Ig_c2; 11.
DR SMART: SM00410; Ig_Like; 5.
DR SMART: SM00281; Lamb; 2.
DR SMART: SM00192; LDla; 3.
DR SMART: SM00018; P_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_4.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLA_1; 3.
DR PROSITE: PS00068; LDLA_2; 3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Alternative splicing; EGF-like domain; Glycoprotein;
KW Hypothetical protein; Laminin EGF-like domain; Repeat.
SQ SEQUENCE 2482 AA; 270943 MW; B24096F7DB694D70 CRC64;

Query Match 39.5%; Score 64; DB 5; Length 2482;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 8 IGEPLVKCK--GAPKKPQRLFM 29
Db 1990 VGEPLQVKEAFGAPGDPPEVEM 2013)

RESULT 6
ID 09XT15 PRELIMINARY; PRT: 3375 AA.
AC 09XT15;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
UN 01-NOV-2001 (TrEMBLrel. 17, last annotation update)
GN UNC-52 OR ZC101.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Percy C., Baynes C.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS: ISOFORM ZC101.2A (09XT15),
CC ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (09XTD2) AND ISOFORM
CC ZC101.2E (SHOWN HERE); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
CC (LDLRA) DOMAIN.
DR EMBL: Z93395; CAB07708.1; JOINED.
DR EMBL: Z93375; CAB07708.1; JOINED.
DR EMBL: Z93375; CAB07569.1; JOINED.
DR EMBL: Z93395; CAB07569.1; JOINED.
DR HSSP: P01130; ILDR.
DR WormRep: ZC101.2E; CE18424.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR000519; P_trefoll.
DR Pfam: PF00047; Ig_17.
DR Pfam: PF00052; Laminin_B_2.
DR Pfam: PF00053; Laminin_EGF_5.
DR Pfam: PF00057; Laminin_G_2.
DR ProDom: PD003031; Laminin_B_2.
DR SMART: SM00180; EGF_Lam; 5.
DR SMART: SM00001; EGF_Like; 3.
DR SMART: SM00408; Ig_c2; 12.
DR SMART: SM00410; Ig_Like; 5.
DR SMART: SM00281; Lamb; 2.
DR SMART: SM00282; LamG; 3.
DR SMART: SM00192; LDla; 3.
DR SMART: SM00018; P_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_7.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLA_1; 3.
DR PROSITE: PS00068; LDLA_2; 3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Alternative splicing; EGF-like domain; Glycoprotein;
KW Hypothetical protein; Laminin EGF-like domain; Repeat.
SQ SEQUENCE 3375 AA; 369049 MW; IAA418BBAE5D67AA CRC64;

Query Match 39.5%; Score 64; DB 5; Length 3375;

Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1

QY 8 IGEPLVCK--GADKPPQLEW 29
:111:111:111:111:
Db 1990 VCEPIQVCKCEARGADPEPEVEM 2013

RESULT 7
Q9V4Y0 PRELIMINARY; PRT: 1482 AA.
AC Q9V4Y0 Q9V4Y1 Q9V4Y2 Q9V4Y3 Q9V4Y4 Q9V4Y5 Q9V4Y6;
01-MAY-2000 (TrEMBLrel. 13. Created)
DT 01-OCT-2000 (TrEMBLrel. 15. Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17. Last annotation update)
DE SNS OR CG3285 OR CG8278 OR CG12495 OR CG13752 OR CG13753 OR CG13754 OR
CG13755 OR CG18464.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RX MEDLINE=20317033; PubMed=10855168;
RP Bour B.A., Chakrivarti M., West J.M., Abmayr S.M.;
RT "Drosophila SNS, a member of the immunoglobulin superfamily that is
RL essential for myoblast fusion.";
RN Genes Dev. 14:1498-1511(2000).
[2]
RP SEQUENCE OF 1-224: 334-477; 491-1061 AND 1274-1482 FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers J., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Buttlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazzolo M., Plutem G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
EMBL: AF254867; AAF77184.1; -

DR	EMBL:	AE003835;	AAF59037.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59038.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59039.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59040.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59041.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59042.1;	ALT_SEQ.
DR	EMBL:	AE003835;	AAF59043.1;	ALT_SEQ.
DR	FlyBase:	FBgn0024189;	sns.	
DR	InterPro:	IPR003961;	FN_1it.	
DR	InterPro:	IPR003598;	I9_c2.	
DR	InterPro:	IPR003600;	I9_1like.	
DR	SMART:	SM00060;	FN3; 1.	
DR	SMART:	SM00408;	IGC2; 4.	
DR	SMART:	SM00410;	IG_1like; 4.	
FT	CONFLICT	28	29	MISSING (IN REF. 2).
FT	CONFLICT	622	622	E-> EA1WOLEACPSOPAMDLPAPVHFAGARPHDNIRE ACOSLKRPEFLRTHTSYLLPACPRIKCPPTGTPMQ
FT	CONFLICT	865	865	PT (IN REF. 2).
FT	CONFLICT	872	872	C -> F (IN REF. 2).
FT	CONFLICT	1402	1402	A -> T (IN REF. 2).
SO	SEQUENCE	1482 AA;	162163 MW;	MISSING (IN REF. 2).
				100CT30FAIPA5397 CRC64;
	Query Match	Best Local Similarity	38.9%;	Score 63; DB 5; Length 1462;
	Matches	10; Conservative	41.7%;	Pred. No. 1.1;
			5; Mismatches	9; Indels
				0; Gaps
Oy	6	ARIGEPLVYKCCKGAPPKKPPORLEW	29	
Db	393	ARVGDIIVPLTCTTAPSNPPEIKW	416	
	: : : : : : :			
RESULT	8			
G9VAJ9	ID	PRELIMINARY:	PRT:	2016 AA.
AC	G9VAJ9:			
DT	01-MAY-2000 (TREMBLrel. 13,			Created)
DT	01-MAY-2000 (TREMBLrel. 13,			Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17,			Last annotation update)
DE	CGI7800 PROTEIN.			
CN	DSCAM OR CGI7800.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
CC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY;			
RX	MEDLINE=20196606; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	Georgie R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Bridton R.C., Rogers Y.-H.C., Blazer R.G., Champé M., Pfeiffer B.D.,			
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.T., Benos P.V., Bernin B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Butteris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cavley S., Dahlke C., Daveenko L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dutdin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,			
RA	Jatalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarly B., Murphy L., Murny D.M., Nelson D.L.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AE003841; AAF59271.1; -.
 DR HSSP: PA0189; LBOU.
 DR FlyBase: FBgn0033159; Dscam.
 DR InterPro: IPR000267; Asparaginse-glutamase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 6.
 DR Pfam: PF00047; Ig; 10.
 DR SMART: SM00060; FN3; 6.
 DR SMART: SM00408; Ig_c2; 7.
 DR SMART: SM00410; Ig_1like; 2.
 DR PROSITE: PS00144; ASN_GLM_ASE_1; UNKNOWN_1.
 SO SEQUENCE 2016 AA; 222109 MW; 6A48DE3B7BD0ABD CRC64;

Query Match 37.7%; Score 61; DB 5; Length 2016;
 Best Local Similarity 54.5%; Pred. No. 3.1;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 2 QNTARIGEPLVLCCKGAPKRP 23
 Db 819 RNOYARRGEPVAVLQCEAKGKRP 840

RESULT 9
 Q9NBA1 PRELIMINARY; PRT; 2016 AA.
 AC Q9NBA1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE DSCAM PRECURSOR.
 GN DSCAM OR CG17800.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RX MEDLINE=20348742; PubMed=10892653;
 RA Schumaker D., Clemens J.C., Shu H., Morby C.A., Xiao J., Mada M.,
 RA Dixon J.E., Zibursky S.L.;
 RT "Drosophila Dscam is an Axon Guidance Receptor Exhibiting
 RT Extraordinary Molecular Diversity.";
 RL Cell 101:671-684(2000).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF260530; AAF71926.1; -.
 DR FlyBase: FBgn0033159; Dscam.
 DR InterPro: IPR000267; Asparaginse-glutamase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003598; Ig_c2.

DR InterPro: IPR003600; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 6.
 DR Pfam: PF00047; Ig; 10.
 DR SMART: SM00060; FN3; 6.
 DR SMART: SM00408; Ig_c2; 7.
 DR SMART: SM00410; Ig_1like; 3.
 DR PROSITE: PS00144; ASN_GLM_ASE_1; UNKNOWN_1.
 KW signal.
 FT SIGNAL.
 SQ SEQUENCE 2016 AA; 222124 MW; 95CF95488F2AD36C CRC64;
 POTENTIAL.
 Query Match 37.7%; Score 61; DB 5; Length 2016;
 Best Local Similarity 54.5%; Pred. No. 3.1;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 2 QNTARIGEPLVLCCKGAPKRP 23
 Db 819 RNOYARRGEPVAVLQCEAKGKRP 840

RESULT 10
 Q9V787 PRELIMINARY; PRT; 1215 AA.
 AC Q9V787; Q9U3Y6.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HIBRIS PROTEIN.
 GN HBS OR CG7449.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarly B., Murphy L., Murny D.M., Nelson D.L.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF210316; AAF19446.1; ALT_INIT.
 DR EMBL: AEO03812; AAF58172.2; -.
 DR FLYBASE: FBgn0029082; hbs.
 DR InterPro: IPR003961; FN11.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 9.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IgC2; 3.
 DR SMART: SM00410; Ig_Like; 6.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
 SQ SEQUENCE 1215 AA; 132053 MW; 62CD064968141C9F CRC64;

Query Match 35.8%; Score 58; DB 5; Length 1215;
 Best Local Similarity 37.5%; Pred. No. 5.1;
 Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 6 ARIGEPVLKCKGAPKPPQRLFW 29
 Db 337 AKYGDVQLSCVTRAPNPQARISH 360

RESULT 11
 ID 09N5C2 PRELIMINARY; PRT; 1791 AA.
 AC 09N5C2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE W06H8.3 PROTEIN.
 GN W06H8.3.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; *Caenorhabditis*.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wilson R.;
 RT "The sequence of *C. elegans* cosmid W06H8.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AC006695; AAF39981.1; -.
 DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00408; IgC2; 2.
 DR SMART: SM00410; Ig_Like; 3.
 SQ SEQUENCE 1791 AA; 199071 MW; 59A9761BCB8B20DA CRC64;

Query Match 34.9%; Score 56.5; DB 5; Length 1791;
 Best Local Similarity 48.1%; Pred. No. 13;
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
 Qy 3 NITRIGEPVLKCKGAPKPPQRLFW 29
 Db 1708 NCEGRIGEPVQLKCLGMPQPE-IEW 1733

RESULT 12
 ID 092626 PRELIMINARY; PRT; 1496 AA.
 AC 092626;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE MYELOBLAST KIAA0230 (FRAGMENT).
 DE KIAA0230.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RX MEDLINE=97191544; PubMed=9039502;
 RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,
 RA Tanaka A., Kotani H., Miyajima N., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI.
 RT The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
 RT analysis of cDNA clones from cell line KG-1 and brain.";
 RL DNA Res. 3:321-329(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MELANOMA;
 RX MEDLINE=95048383; PubMed=7959781;
 RA Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,
 RA Trent J.M.;
 RT "Assignment of a human melanoma associated gene MG50 (D2S448) to
 RT chromosome 2p25.3 by fluorescence in situ hybridization.";
 RL Genomics 22:243-244(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MELANOMA;
 RA Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J.;
 RT "Identification of a novel melanoma gene (MG50) - likely the gene for
 RT IL-1 receptor antagonist - which encodes epitopes recognized by human
 RT cytolytic T lymphocytes.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: D86983; BAA13219.1; -.
 DR EMBL: AF200348; AAF06354.1; -.
 DR HSSP: P05164; IXP.
 DR InterPro: IPR002007; Anln_peroxidase.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_typ.
 DR InterPro: IPR001536; Peroxidase_3.
 DR InterPro: IPR002016; Peroxidase.
 DR InterPro: IPR001007; VMFC.
 DR Pfam: PF00047; Ig; 4.

DR Pfam: PF00560; LRR; 5.
 DR Pfam: PF01463; LRRT; 1.
 DR Pfam: PF00141; peroxidase; 1.
 DR Pfam: PF00093; vwc; 1.
 DR PRINTS: PR00457; ANPEROXIDASE.
 DR SMART: SM00408; Igc2; 4.
 DR SMART: SM00082; LRRT; 1.
 DR SMART: SM00013; LRRT; 1.
 DR SMART: SM00369; LRR_TYP; 4.
 DR PROSITE: PS01208; vWFC; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 1496 AA; 167209 MW; E9B9A7069BF1ABFF CRC64;

Query Match 34.3%; Score 55.5; DB 4; Length 1496;
 Best Local Similarity 39.3%; Pred. No. 15;
 Matches 11; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 2 ONITARIGEPVLKCKGAPKPPORLEW 29
 DB 366 QNTEVLVGESEVLEEC-SATGHPPRISW 392

RESULT 13
 ID 025198 PRELIMINARY; PRT: 848 AA.
 AC 025198:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE RECEPTOR TYROSINE KINASE 90.
 GN HTK90.
 OS Hydra attenuata (Hydra) (Hydra vulgaris)
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
 OC Hydridae; Hydra.
 OX NCBITaxID=6087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miller M.A., Steele R.E.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
 CC EMBL: U59448; AAB03389.1; -.
 DR HSSP: P06213; IIRK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR01245; Tyr_kin.
 DR Pfam: PF00047; Ig_5.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; Igc2; 2.
 DR SMART: SM00410; Ig_Like; 3.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 848 AA; 95551 MW; D0A52ED6A8760C07 CRC64;

Query Match 34.0%; Score 55; DB 5; Length 848;
 Best Local Similarity 59.1%; Pred. No. 9.8;
 Matches 13; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 2 ONITARIGEPVLKCK--KGAPK 21
 DB 422 KNITATIGEPANVHCCKGKFPK 443

RESULT 14

092214
 ID 092214 PRELIMINARY; PRT: 1344 AA.
 AC 092214:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE RIG-1 PROTEIN.
 GN RBIG1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
 CC EMBL: AF060570; AAD11628.1; -.
 DR HSSP: P56276; ITLK.
 DR MGD: MGI:1343102; RBIG1.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00047; Ig_5.
 DR SMART: SM00060; FN3; 3.
 DR SMART: SM00408; Igc2; 5.
 SQ SEQUENCE 1344 AA; 143439 MW; 8B0060341C49CFEA CRC64;

Query Match 33.3%; Score 54; DB 11; Length 1344;
 Best Local Similarity 32.1%; Pred. No. 22;
 Matches 9; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 3 NITARIGEPVLKCKGAPKPPORLEW 30
 DB 152 NVYVAVGEPAVMCEVPPKGPHEPLVTWK 179

RESULT 15
 ID 090F14 PRELIMINARY; PRT: 483 AA.
 AC 090F14:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE HYPOTHETICAL 51.9 KDA PROTEIN (FRAGMENT).
 GN DKFZP58601624.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBITaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
 CC EMBL: AL117666; CAB56036.1; -.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00408; Igc2; 2.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 483 AA; 51907 MW; B3DFEC945C0DF8FC CRC64;

Query Match 33.0%; Score 53.5; DB 4; Length 483;
 Best Local Similarity 45.5%; Pred. No. 9.2;
 Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Wed Apr 24 09:48:11 2002

us-09-689-469-5.rspt

Page 8

```
QY      8 IGEPLVLCKCKGAPKKPPQRLEW 29
      :|| : ||| | ||| : |
Db     96 VGETVALQCK-ATGNPPPRITW 116
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Search completed: April 24, 2002, 09:20:13
Job time: 242 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:51 ; Search time 66.52 Seconds
(without alignments)
11.135 Million cell updates/sec

Title: US-09-689-469-6

Perfect score: 10

Sequence: 1 AONITARIGE 10

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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20: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:*
21: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:*
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	20	AAV09353
2	10	100.0	10	21	AAV52135
3	10	100.0	15	18	AAW44208
4	10	100.0	15	18	AAW33762
5	10	100.0	16	18	AAW44214
6	10	100.0	16	18	AAW33768
7	10	100.0	30	20	AAV09349
8	10	100.0	30	21	AAV52134
9	10	100.0	318	18	AAW44200
10	10	100.0	318	18	AAW33754
11	10	100.0	332	21	AAV52130

12	10	100.0	340	18	AAW44199
13	10	100.0	340	18	AAW33753
14	10	100.0	404	22	AAW81925
15	9	90.0	30	20	AAV09350
16	9	90.0	30	20	AAV09351
17	8	80.0	30	20	AAV09352
18	6	60.0	30	18	AAW23337
19	6	60.0	369	21	AAW52004
20	6	60.0	400	21	AAW52003
21	6	60.0	452	21	AAW52002
22	6	60.0	456	21	AAW20758
23	6	60.0	456	21	AAW50449
24	6	60.0	481	21	AAW20757
25	6	60.0	481	21	AAW50448
26	6	60.0	548	21	AAW20755
27	6	60.0	548	21	AAW50447
28	6	60.0	741	17	AAW89327
29	6	60.0	788	22	AAW88505
30	5	50.0	5	21	AAV90767
31	5	50.0	30	22	AAW05141
32	5	50.0	44	21	AAW08055
33	5	50.0	45	21	AAW33101
34	5	50.0	50	21	AAW22634
35	5	50.0	54	22	AAW20409
36	5	50.0	54	22	AAW34894
37	5	50.0	61	21	AAW08913
38	5	50.0	69	21	AAW32098
39	5	50.0	69	21	AAW44665
40	5	50.0	69	21	AAW08054
41	5	50.0	69	21	AAW00645
42	5	50.0	70	21	AAW22559
43	5	50.0	70	21	AAW33100
44	5	50.0	70	21	AAW64760
45	5	50.0	72	19	AAW75093

ALIGNMENTS

RESULT 1	
ID AAV09353	standard; peptide: 10 AA.
XX AAV09353;	
DT 09-JUL-1999	(first entry)
XX	
XX	
DE Human RAGE V-domain	peptide SEQ ID NO:5.
XX	
KW RAGE: V-domain; receptor for advanced glycation endproduct;	
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;	
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;	
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;	
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;	
KW tumour; cancer; male impotence; wound healing; periodontal disease;	
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.	
XX	
OS Homo sapiens.	
XX	
PN W09918987-A1.	
XX	
PD 22-APR-1999.	
XX	
PF 09-OCT-1998;	98WO-US21346.
XX	
PR 09-OCT-1997;	97US-0948131.
XX	
PA (UYCO) UNIV COLUMBIA NEW YORK.	
XX	
PI Lamster I, Schmidt AM, Stern D, Yan SD;	
DR WPI; 1999-277439/23.	
XX	

PT New peptides based on an advanced glycation end product receptor are
 PT useful for treating Alzheimer's disease and Down's syndrome
 XX
 PS Claim 55: Page 85; 101pp; English.

XX The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC v-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC extracellular formation of an ABP fibril on a cell; (4) inhibiting
 CC aggregation of ABP on the surface of a cell; (5) inhibiting
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
 | | | | | | | | | |
 Db 1 agnitarige 10

RESULT 2

AA52135
 ID AAY52135 standard; peptide; 10 AA.

XX
 AC AAY52135;

XX
 DT 28-JAN-2000 (first entry)

XX
 DE Human Receptor to AGE (RAGE) amino acid sequence fragment #4.

XX
 KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 KW invasion; metastasis; amphotericin; neuron; inhibit; therapy.

XX
 OS Homo sapiens.

XX
 PN WO954485-A1.

XX
 PD 28-OCT-1999.

XX
 PF 16-APR-1999; 99WO-US08427.

XX
 PR 17-APR-1998; 98US-0062365.

XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX
 PI Schmidt AM, Stern D;

XX
 DR WPI; 2000-013260/01.

XX
 PT Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts
 XX
 PS Claim 30: Page 62; 88pp; English.

XX This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphotericin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphotericin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
 | | | | | | | | | |
 Db 1 agnitarige 10

RESULT 3

AAW44208
 ID AAW44208 standard; peptide; 15 AA.

XX
 AC AAW44208;

XX
 DT 14-MAY-1998 (first entry)

XX
 DE Human soluble RAGE immunologically active fragment SEQ ID NO:12.

XX
 KW Human: soluble receptor; advanced glycosylation end product; RAGE;
 KW AGE; antibody; vascular permeability; immunologically active fragment;
 KW diabetes mellitus.

XX
 OS Homo sapiens.

XX
 PN WO9739125-A1.

XX
 PD 23-OCT-1997.

XX
 PF 11-APR-1997; 97WO-EP01834.

XX
 PR 16-APR-1996; 96US-0633148.

XX
 PA (SCHMID) SCHERING PATENTE AG.

XX
 PI Hollander DA, Morser MJ, Nagashima M;

XX
 DR WPI; 1997-558580/51.

XX
 PT Anti-advanced glycosylation end product polypeptide antibody
 PT prevents receptor binding and therefore reduces vascular
 PT permeability, useful to treat diabetes mellitus
 XX
 PS Claim 2: Page 46; 90pp; English.

XX The present sequence represents an immunologically active fragment
 CC of a soluble human receptor to an advanced glycosylation end
 CC product (RAGE) polypeptide. The present invention describes

CC an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 Db 1 agptarige 10

RESULT 4
 AAW33762

ID AAW33762 standard; peptide; 15 AA.

AC AAW33762;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 8.

KM Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KM Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

PT New soluble advanced glycosylation end-product receptor polypeptide
 PT - used for reducing vascular permeability, complications of diabetes
 PT etc., also for purification and to screen for modulators
 PS Claim 6; Page 55; 91pp; English.

CC This is a peptide fragment of a human advanced glycosylation end-product
 CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active
 CC fragments or their mimetics can inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, atherosclerosis or
 CC retinopathy) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 Db 1 agptarige 10

RESULT 5

ID AAW44214 standard; peptide; 16 AA.

AC AAW44214;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.

KM Human; soluble receptor; advanced glycosylation end product; RAGE;
 KM AGE; antibody; vascular permeability; immunologically active fragment;
 KM diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody -
 PT prevents receptor binding and therefore reduces vascular
 PT permeability, useful to treat diabetes mellitus
 PS Claim 2; Page 49; 90pp; English.

CC The present sequence represents an immunologically active fragment
 CC of a soluble human receptor to an advanced glycosylation end
 CC product (RAGE) polypeptide. The present invention describes
 CC an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 16 AA;

Query Match 100.0%; Score 10; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGE 10
Db 1 agnitarige 10

RESULT 6

AAW33768
ID AAW33768 standard; peptide; 16 AA.

AAW33768;

08-MAY-1998 (first entry)

Human RAGE polypeptide fragment 14.

Advanced glycosylation end-product receptor; RAGE; screening; AGE;
vascular permeability; diabetes mellitus; treatment; atherosclerosis;
Alzheimer's disease.

Homo sapiens.

WO9739121-A1.

23-OCT-1997.

11-APR-1997; 97WO-EP01832.

16-APR-1996; 96US-0633147.

(SCHD) SCHERING AG.

Morser MJ, Nagashima M;

WPI; 1997-526458/48.

New soluble advanced glycosylation end-product receptor polypeptide
- used for reducing vascular permeability; complications of diabetes
etc., also for purification and to screen for modulators

Disclosure: Page 9, 91pp; English.

This is a peptide fragment of a human advanced glycosylation end-product
receptor (RAGE) polypeptide. The RAGE polypeptides and its active
fragments or their mimetics can inhibit interaction between advanced
glycosylation end-products (AGE) and a receptor (specifically RAGE). They
are used to treat diseases associated with AGE/RAGE interaction, such as
increased vascular permeability, diabetes mellitus (particularly
complications such as micro- or macro- vasculopathy or occlusive vascular
disease) or haemodialysis-associated amyloidosis, also activation
of microglial cells by beta-amyloid peptides in Alzheimer's disease or
age-related disorders such as oxidative stress. These RAGE polypeptides
are also used, when immobilised, to purify AGE from a protein mixture and
to screen for compounds that are agonists and antagonists of AGE/RAGE
interaction. They can also be used diagnostically to detect abnormal
levels of AGE. Antibodies against RAGE polypeptides are useful as
immunoassay reagents for measurement of RAGE levels, and as inhibitors of
interaction between AGE and RAGE or other receptors and for purification
and quantification of RAGE polypeptides. The encoding nucleic acids are
used to express recombinant RAGE and as probes for isolating related
genes.

Sequence 16 AA:

Query Match 100.0%; Score 10; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGE 10

Db 1 agnitarige 10

RESULT 7

AAV09349
ID AAV09349 standard; peptide; 30 AA.

AAV09349;

09-JUL-1999 (first entry)

Human RAGE V-domain peptide SEQ ID NO:1.

RAGE: V-domain; receptor for advanced glycation endproduct;
ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
neural cytotoxicity; head trauma; amyotrophic lateral sclerosis;
multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
tumour; cancer; male impotence; wound healing; periodontal disease;
neuropathy; retinopathy; nephropathy; neuronal degeneration.

Homo sapiens.

WO9918987-A1.

22-APR-1999.

09-OCT-1998; 98WO-US21346.

09-OCT-1997; 97US-0948131.

(UYCO) UNIV COLUMBIA NEW YORK.

Lamster I, Schmidt AM, Stern D, Yan SD;

WPI; 1999-277439/23.

New peptides based on an advanced glycation end product receptor are
useful for treating Alzheimer's disease and Down's syndrome

Claim 2; Page 78; 101pp; English.

The present invention describes novel isolated peptides (I) having an
amino acid sequence corresponding to an amino acid sequence of a
V-domain of a receptor for an advanced glycation end product (RAGE).
Also described are methods for: (1) inhibiting an amyloid-beta peptide
(ABP) interaction with a receptor for RAGE when the receptor is on the
surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
inhibiting formation of an ABP fibril on a cell; (4) inhibiting
extracellular assembly of an ABP into a fibril; (5) inhibiting
aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
of a microglial cell into senile plaques; (7) inhibiting activation of a
microglial cell by an ABP; (8) treating a subject with a condition
associated with an interaction of an ABP with a receptor for RAGE on a
cell; (9) evaluating the ability of an agent to inhibit binding of an
ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
periodontal disease in a subject; (12) inhibiting an RAGE's interaction
with a receptor for RAGE when the receptor is on the surface of a cell;
and (13) treating a subject with a condition associated with an
interaction of an RAGE with a receptor for RAGE on a cell. The methods
can be used for treating conditions associated with an interaction of an
ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
disease, senility, renal failure, hyperlipidaemic atherosclerosis,
neural cytotoxicity, Down's syndrome, dementia associated with head
trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
an autoimmune disease, inflammation, a tumour, cancer, male impotence,
wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
or neuronal degeneration.

Sequence 30 AA:

XX

Query Match 100.0%; Score 10; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 Db 1 aqntarige 10

RESULT 8

AAV52134
 ID AAV52134 standard; protein; 30 AA.

AC AAV52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KM Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN W0954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

PT Inhibiting tumour invasion or spreading by administration of soluble
 receptor for advanced glycation endproducts -

PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAV52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 10; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 Db 1 aqntarige 10

RESULT 9

AAW44200
 ID AAW44200 standard; Protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KM Human; soluble receptor; advanced glycosylation end product; RAGE;
 AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 66 /note= "encoded by CCT"

PN W09739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

DT N-PSDB; AAV12395.

PT Anti-advanced glycosylation end product polypeptide antibody -
 PT prevents receptor binding and therefore reduces vascular
 PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

CC The present sequence represents a mature human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 318 AA;

Query Match 100.0%; Score 10; DB 18; Length 318;

Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 Db 1 aqntarige 10

RESULT 10

AAW3754
 ID AAW3754 standard; Protein; 318 AA.

AC AAW3754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

XX	Homo sapiens.
OS	
XX	MO9954485-A1.
PN	
PD	28-OCT-1999.
XX	
PF	16-APR-1999; 99WO-US08427.
XX	
PR	17-APR-1998; 98US-0062365.
XX	
PA	(UYCO) UNIV COLUMBIA NEW YORK.
XX	
PI	Schmidt AM, Stern D;
XX	
DR	WPL: 2000-013260/01.
XX	
PT	Inhibiting tumour invasion or spreading by administration of soluble
XX	receptor for advanced glycation endproducts -
PS	Disclosure: Page 10-11; 88pp; English.
XX	
CC	This is the amino acid sequence of the human soluble Receptor for
CC	Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of
CC	physiologically and pathophysiologically relevant ligands when
CC	considering tumour invasion. In normal developing neurons RAGE
CC	colocalizes with amphoterin which is a matrix associated polypeptide.
CC	The expression of both RAGE and amphoterin decreases after birth, but
CC	both have increased expression in tumours. RAGE polypeptides
CC	AAY52132-752135 are used in the invention in a method for inhibiting
CC	tumour invasion and metastasis. The method involves inhibiting tumour
CC	invasion and metastasis via administration of a therapeutically effective
CC	amount of the pharmaceutical composition containing a RAGE polypeptide.
CC	The invention also relates to a method for evaluating the ability of an
CC	agent to inhibit tumour invasion in a local cellular environment. RAGE
CC	can be administered to a patient in a pharmaceutically acceptable
CC	carrier.
XX	
SQ	Sequence 332 AA:
Query Match	100.0%; Score 10; DB 21; Length 332;
Best Local Similarity	100.0%; Pred. No. 0.002;
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
OY	I AONTIRARIGE 10
DB	1 agnitarige 10
RESULT 12	
AAW44199	
ID	AAW44199 standard; Protein; 340 AA.
XX	
CC	AAW44199;
XX	
DT	14-MAY-1998 (first entry)
XX	
DE	Human soluble receptor to an advanced glycosylation end product.
XX	
KW	Human; soluble receptor; advanced glycosylation end product; RAGE;
XX	AGE; antibody; vascular permeability; diabetes mellitus.
XX	
OS	Homo sapiens.
XX	
PN	MO9739125-A1.
XX	
PD	23-OCT-1997.
XX	
PF	11-APR-1997; 97WO-Ep01834.
XX	
PR	16-APR-1996; 96US-0633148.
XX	

PA (SCHD) SCHERING PATENTE AG.
 XX
 PI Hollander DA, Morser MJ, Nagashima M;
 XX WPI; 1997-556580/51.
 DR N-PSDB; AAV12394.
 XX
 PI Anti-advanced glycosylation end-product polypeptide antibody -
 PT prevents receptor binding and therefore reduces vascular
 PI permeability, useful to treat diabetes mellitus
 XX
 PS Claim 2; Page 40-41; 90pp; English.
 XX
 CC The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end-product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end-products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.
 CC
 SQ Sequence 340 AA;

Query Match 100.0%; Score 10; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||
 Db 23 agnitarige 32

RESULT 13
 AAW33753
 ID AAW33753 standard; Protein; 340 AA.
 XX
 AC AAW33753;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Human RAGE polypeptide (340 amino acid residues).
 XX
 KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9739121-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-EP01832.
 XX
 PR 16-APR-1996; 96US-0633147.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Morser MJ, Nagashima M;
 XX WPI; 1997-526458/48.
 DR N-PSDB; AAV06517.
 XX
 PT New soluble advanced glycosylation end-product receptor polypeptide
 PT - used for reducing vascular permeability, complications of diabetes
 PT etc., also for purification and to screen for modulators
 XX

PS Claim 3; Fig 1A; 91pp; English.

XX
 CC This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro-vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.
 CC
 SQ Sequence 340 AA;

Query Match 100.0%; Score 10; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||
 Db 23 agnitarige 32

RESULT 14
 AAB81925
 ID AAB81925 standard; protein; 404 AA.
 XX
 AC AAB81925;
 XX
 DT 15-JUN-2001 (first entry)
 XX
 DE Extracorporeal circulation material receptor protein.
 XX
 DE Extracorporeal circulation; carbonyl stress product; receptor;
 KW diabetes; vascular lesion; excretory dysfunction.
 XX
 OS Unidentified.
 XX
 PN WO200118060-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-JP06172.
 XX
 PR 08-SEP-1999; 99JP-0254463.
 XX
 PA (TORA) TORAY IND INC.
 XX
 PI Shimizu S, Kubota M, Akiyama H, Usui M;
 XX WPI; 2001-290314/30.
 DR
 XX
 PT Material for extracorporeal circulation, applicable in selective
 PT elimination of diabetic complication factors such as carbonyl stress
 PT products caused by abnormally promoted carbonyl stress from excretory
 PT dysfunction in vascular lesions -
 XX
 PS Claim 1; Page 31-32; 36pp; Japanese.
 XX
 CC The present invention describes a material for extracorporeal circulation
 CC which is made from a water-insoluble carrier immobilized with a protein

CC having the sequence shown here. The materials of the invention, including
 CC adsorbents, are for extracorporeal circulation, which are applicable in
 CC the selective elimination of diabetic complication factors from a body
 CC fluid, and are therefore useful in treating vascular lesions like
 CC arteriosclerosis due to carbonyl stress products caused by abnormally
 CC promoted carbonyl stress from excretory dysfunction.
 XX
 SO Sequence 404 AA:

QY 1 AONTARIGE 10
 Db 23 agntarige 32

Query Match 100.0%; Score 10; DB 22; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.0023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 AAY09350
 ID AAY09350 standard; peptide; 30 AA.
 AC AAY09350;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Mouse RAGE V-domain peptide SEQ ID NO:2.
 XX
 KW RAGE: V-domain; receptor for advanced glycation endproduct;
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW tumour; cancer; male impotence; wound healing; periodontal disease;
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.
 XX
 OS Mus sp.
 XX
 PN W09918987-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21346.
 XX
 PR 09-OCT-1997; 97US-0948131.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Lamster I, Schmidt AM, Stern D, Yan SD;
 XX
 DR WPI; 1999-277439/23.
 XX
 PT New peptides based on an advanced glycation end product receptor are
 XX useful for treating Alzheimer's disease and Down's syndrome
 PS
 XX Claim 3; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting

CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 XX
 SO Sequence 30 AA;

QY 2 ONITARIGE 10
 Db 2 qntarige 10

Query Match 90.0%; Score 9; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 24, 2002, 09:21:51
 Job time: 250 sec

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OM protein -- protein search, using sw model

Run on: April 24, 2002, 09:22:30 ; Search time 32.21 Seconds
(without alignments)
6.986 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 10
Sequence: 1 AONTARIGE 10

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	15	US-08-633-148-12	Sequence 12, Appl
2	10	100.0	16	US-08-633-148-18	Sequence 18, Appl
3	10	100.0	318	US-08-633-148-4	Sequence 4, Appl
4	10	100.0	340	US-08-633-148-2	Sequence 2, Appl
5	6	60.0	741	US-08-277-231A-4	Sequence 4, Appl
6	6	60.0	741	US-08-473-750-7	Sequence 7, Appl
7	6	60.0	741	US-08-477-326-7	Sequence 7, Appl
8	5	50.0	63	US-08-637-759B-191	Sequence 191, App
9	5	50.0	63	US-08-871-355A-191	Sequence 191, App
10	5	50.0	72	US-09-188-930-153	Sequence 153, App
11	5	50.0	72	US-09-188-930-304	Sequence 304, App
12	5	50.0	146	US-08-543-238-11	Sequence 11, Appl
13	5	50.0	146	US-08-420-526-11	Sequence 11, Appl
14	5	50.0	198	US-08-278-091-16	Sequence 16, Appl
15	5	50.0	198	US-08-483-859-16	Sequence 16, Appl
16	5	50.0	198	US-08-472-173-16	Sequence 16, Appl
17	5	50.0	198	US-08-487-167-16	Sequence 16, Appl
18	5	50.0	198	US-08-483-816-16	Sequence 16, Appl
19	5	50.0	198	US-08-296-149-16	Sequence 16, Appl
20	5	50.0	198	US-08-801-499-16	Sequence 16, Appl
21	5	50.0	198	US-08-615-271-16	Sequence 16, Appl
22	5	50.0	198	US-09-074-660-16	Sequence 16, Appl
23	5	50.0	198	US-09-074-659-16	Sequence 16, Appl
24	5	50.0	198	US-09-106-468-16	Sequence 16, Appl
25	5	50.0	198	US-09-106-468A-16	Sequence 16, Appl
26	5	50.0	198	US-09-106-467-16	Sequence 16, Appl
27	5	50.0	236	PCT-US91-08177-17	Sequence 17, Appl

28	5	50.0	241	5	PCT-US91-08177-7	Sequence 7, Appl
29	5	50.0	305	4	US-09-248-588-11	Sequence 11, Appl
30	5	50.0	305	4	US-09-248-588-13	Sequence 13, Appl
31	5	50.0	352	3	US-08-967-272-2	Sequence 2, Appl
32	5	50.0	373	1	US-07-723-002C-2	Sequence 2, Appl
33	5	50.0	379	1	US-07-723-002C-4	Sequence 4, Appl
34	5	50.0	379	2	US-07-723-002C-6	Sequence 6, Appl
35	5	50.0	379	2	US-08-887-365-36	Sequence 36, Appl
36	5	50.0	397	1	US-07-956-697B-5	Sequence 5, Appl
37	5	50.0	397	1	US-08-263-098-5	Sequence 5, Appl
38	5	50.0	420	5	PCT-US96-10602-10	Sequence 10, Appl
39	5	50.0	439	3	US-08-993-359-24	Sequence 24, Appl
40	5	50.0	439	3	US-09-221-654-2	Sequence 2, Appl
41	5	50.0	439	3	US-08-989-358A-2	Sequence 2, Appl
42	5	50.0	453	4	US-09-013-881-5	Sequence 5, Appl
43	5	50.0	461	2	US-08-630-822A-68	Sequence 68, Appl
44	5	50.0	461	2	US-09-005-069-68	Sequence 68, Appl
45	5	50.0	507	1	US-08-097-829-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-633-148-12
Sequence 12, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: MORPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-12
Query Match 100.0%; Score 10; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AONTARIGE 10
|||||||

Db 1 AONITARIGE 10

RESULT 2

US-08-633-148-18
Sequence 18, Application US/08633148
Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-18

Query Match

Best Local Similarity 100.0%; Score 10; DB 2; Length 16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 3

US-08-633-148-4

Sequence 4, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-4

Query Match

Best Local Similarity 100.0%; Score 10; DB 2; Length 318;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 4

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 100.0%; Score 10; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGE 10
|||||
DB 23 AONTARIGE 32

RESULT 5
US-08-277-231A-4
Sequence 4, Application US/08277231A
Patent No. 5643725
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP P11n
Patent No. 5643725
TITLE OF INVENTION: Structural Genes and the LKP P11 Operon of No. 5643725typable
TITLE OF INVENTION: Haemophilus Influenzae
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277.231A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 32,542
REFERENCE/DOCKET NUMBER: ACC94-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-277-231A-4

Query Match 60.0%; Score 6; DB 1; Length 741;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
|||||
DB 157 TARIGE 162

RESULT 6
US-08-473-750-7
Sequence 7, Application US/08473750
Patent No. 5834187

Patent No. 5834187 5786143
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP P11n
Patent No. 5834187
TITLE OF INVENTION: Structural Gene and the LKP P11 Operon of No. 5834187 5786
TITLE OF INVENTION: Haemophilus Influenzae
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473.750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,321
FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-750-7

Query Match 60.0%; Score 6; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
|||||
DB 157 TARIGE 162

RESULT 7
US-08-477-326-7
Sequence 7, Application US/08477326
Patent No. 5968769
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP P11n
Patent No. 5968769
TITLE OF INVENTION: Structural Gene and the LKP P11 Operon of No. 5968769typab
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,326
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/277,231
FILING DATE: July 19, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-326-7

Query Match 60.0%; Score 6; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
111111
Db 157 TARIGE 162

RESULT 8
US-08-637-759B-191
Sequence 191, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-637-759B-191

Query Match 50.0%; Score 5; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNITA 6
11111
Db 28 QNITA 32

RESULT 9
US-08-871-355A-191
Sequence 191, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPS 101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-871-355A-191

Query Match 50.0%; Score 5; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNITA 6
11111

Db 28 ONITA 32

RESULT 10

US-09-188-930-153
; Sequence 153, Application US/09188930A
; Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 153

LENGTH: 72

TYPE: PRT

ORGANISM: mouse

US-09-188-930-153

Query Match

Best Local Similarity 50.0%; Score 5; DB 4; Length 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ARIGE 10

Db 47 ARIGE 51

RESULT 11

US-09-188-930-304
; Sequence 304, Application US/09188930A
; Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 304

LENGTH: 72

TYPE: PRT

ORGANISM: Mouse

US-09-188-930-304

Query Match

Best Local Similarity 50.0%; Score 5; DB 4; Length 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ARIGE 10

Db 47 ARIGE 51

RESULT 12

US-08-543-238-11
; Sequence 11, Application US/08543238
; Patent No. 5607919

GENERAL INFORMATION:

APPLICANT: Bojsen, Kirsten

APPLICANT: Kragh, Karsten M.

APPLICANT: Mikkelsen, Jørn D.

APPLICANT: Nielsen, Klaus K.

TITLE OF INVENTION: Anti-Microbial Proteins

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sandoz Agro, Inc.

STREET: 975 California Avenue

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/543,238

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Marcus-Wyner, Lynn

REGISTRATION NUMBER: 34,869

REFERENCE/DOCKET NUMBER: 137-1078/MA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/354-3588

TELEFAX: 415/857-1125

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-543-238-11

Query Match

Best Local Similarity 50.0%; Score 5; DB 1; Length 146;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARI 8

Db 99 ITARI 103

RESULT 13

US-08-420-526-11
; Sequence 11, Application US/08420526
; Patent No. 5608151

GENERAL INFORMATION:

APPLICANT: Bojsen, Kirsten

APPLICANT: Kragh, Karsten M.

APPLICANT: Mikkelsen, Jørn D.

APPLICANT: Nielsen, Klaus K.

TITLE OF INVENTION: Anti-Microbial Proteins

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sandoz Agro, Inc.

STREET: 975 California Avenue

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/420,526

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1078/MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-420-526-11

Query Match 50.0%; Score 5; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TARIG 8
|||||
DB 99 TARIG 103

RESULT 14
US-08-278-091-16
Sequence 16, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-278-091-16

Query Match 50.0%; Score 5; DB 1; Length 198;

Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIG 9
|||||
DB 43 TARIG 47

RESULT 15
US-08-483-859-16
Sequence 16, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-495 MIS:v9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-859-16

Query Match 50.0%; Score 5; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIG 9
|||||
DB 43 TARIG 47

Search completed: April 24, 2002, 09:22:30
Job time: 249 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:17 ; Search time 38.65 Seconds
(without alignments)
19.709 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 10
Sequence: 1 AONTARIGE 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	404	1	I61596	advanced glycosyla
2	90.0	402	1	T09062	probable advanced
3	80.0	416	1	A42879	advanced glycosyla
4	70.0	223	2	H64065	mutator muth - Hae
5	60.0	234	1	Q0BE43	membrane antigen g
6	60.0	238	2	H64181	ABC-type transport
7	60.0	298	2	T51746	RNA helicase RH17
8	60.0	389	2	S33667	probable integrase
9	60.0	429	2	T23984	hypothetical prote
10	60.0	468	2	H69133	argininosuccinate
11	60.0	471	2	S30585	hypothetical prote
12	60.0	548	2	T05671	hypothetical prote
13	60.0	609	2	G84832	ATP-dependent RNA
14	60.0	635	2	E71733	threonine--tRNA 11
15	60.0	788	2	I64045	recombination prot
16	60.0	837	1	S54429	outer membrane ush
17	50.0	100	2	S68627	p24 protein - born
18	50.0	118	2	D75580	hypothetical 13.7K
19	50.0	124	2	S56506	hypothetical 13.7K
20	50.0	125	2	A53882	Darwin homolog whe
21	50.0	125	2	A43474	Darwin homolog whe
22	50.0	125	2	A83256	conserved hypotet
23	50.0	137	2	T05526	acyl carrier prote
24	50.0	146	2	T06169	pathogenesis-relat
25	50.0	146	2	T06485	barrin homolog whe
26	50.0	147	2	S41381	hypothetical prote
27	50.0	148	2	T06486	Darwin homolog whe
28	50.0	157	2	D84243	hypothetical prote
29	50.0	157	2	S49793	hypothetical prote

30	5	50.0	163	2	S67038	ribosomal protein
31	5	50.0	164	2	H64329	hypothetical prote
32	5	50.0	164	2	S38089	hypothetical prote
33	5	50.0	166	2	A82946	ribosomal protein
34	5	50.0	175	2	JN0681	gamma2-crystallin
35	5	50.0	180	2	S75124	thioredoxin-like p
36	5	50.0	183	2	T10192	senescence-associ
37	5	50.0	185	2	S20593	alcohol dehydrogen
38	5	50.0	186	2	T50361	hypothetical prote
39	5	50.0	190	2	T09136	ADP-ribosylation F
40	5	50.0	196	2	E86553	3-methyladenine DN
41	5	50.0	196	2	C72071	DNA-3-methyladenin
42	5	50.0	197	2	A83092	probable phospho
43	5	50.0	201	2	G70874	probable transcrip
44	5	50.0	204	2	S30165	repressor protein
45	5	50.0	220	2	T51827	MADS-box protein (

ALIGNMENTS

RESULT 1
I61596
advanced glycosylation end-products receptor precursor - human
N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text, change 16-Jul-1999
C:Accession: I61596; B42879; S27968
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.
Genomics 23, 408-419, 1994
A>Title: Three genes in the human MHC class III region near the junction with the class II region part of mouse mammary tumor gene int-3.
A:Reference number: A55562; MIM:95137587
A:Accession: I61596
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-404 <RES>
A:Cross-references: GB:D28769; NID:9561657; PIDN:BA05958.1; PID:9561659
R:Neepfer, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A:Reference number: A42879; MIM:92340547
A:Accession: B42879
A:Molecule type: mRNA
A:Residues: 'G', '2-99', 'R', '101-404' <NE>
A:Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846
A:Experimental source: lung
A:Note: sequence extracted from NCBI backbone (NCBIP:109438)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosylated cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
A:Genetics:
A:Gene: GDB:AGER
A:Cross-references: GDB:306354; OMIM:600214
A:Map position: 6p21.3-6p21.3
A:Intons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C:Superfamily: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <EXT>
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT
F:23-344/Domain: extracellular #status predicted <EXT>
F:31-101/Domain: immunoglobulin homology <IM1>
F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:345-363/Domain: transmembrane #status predicted <IM4>
F:363-404/Domain: intracellular #status predicted <IM5>
F:25-81/Binding site: carboxylate (Asn) (covalent) #status predicted
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

Query Match 100.0%; Score 10; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||

Db 23 AONTARIGE 32

RESULT 2
 T09062
 probable advanced glycosylation end-products receptor precursor - mouse
 N:Alternate names: RAGE
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
 C:Accession: T09062
 R:Rowen, U.; Maniatis, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
 submitted to the EMBL Data Library, October 1997
 A:Description: Sequence of the mouse major histocompatibility locus class III region.
 A:Reference number: 216543
 A:Accession: T09062
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-402 <ROM>
 A:Cross-references: EMBL:AF030001; NID:92564945; PID:92564950
 C:Genetics: RAGE
 A:Gene: RAGE
 A:Map position: 17
 A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
 C:Superfamily: advanced glycosylation end products receptor; Immunoglobulin homology
 C:Keywords: receptor; transmembrane protein
 F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 9; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
 |||||||||

Db 24 ONTARIGE 32

RESULT 3
 A42879
 advanced glycosylation end-products receptor precursor - bovine
 N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
 C:Accession: A42879; A42878; S27949
 R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
 J. Biol. Chem. 267, 14988-15004, 1992
 A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
 A:Reference number: A42879; M0ID:92340547
 A:Accession: A42879
 A:Molecule type: mRNA
 A:Residues: 1-416 <NDE>
 A:Cross-references: GB:M91212; NID:q163650; PIDN:AAA03575.1; PID:q163651
 A:Experimental source: lung
 A>Note: sequence extracted from NCBI backbone (NCBIP:109436)
 A>Note: parts of this sequence, including the amino end of the mature protein, were dete
 R:Schmidt, A.M.; Vienna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
 J. Biol. Chem. 267, 14987-14997, 1992
 A:Title: Isolation and characterization of two binding proteins for advanced glycosylati
 A:Reference number: A42878; M0ID:92340546
 A:Accession: A42878
 A:Molecule type: protein
 A:Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>
 A:Experimental source: endothelial cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:109434)
 C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
 cellular function, thus contributing to tissue lesions in diabetes.
 C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
 C:Function:
 A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
 C:Superfamily: advanced glycosylation end products receptor; Immunoglobulin homology
 C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
 F:23-354/Domain: extracellular #status predicted <EXT>
 F:31-100/Domain: immunoglobulin homology <IMM>
 F:136-209/Domain: immunoglobulin homology <IMM>
 F:262-313/Domain: immunoglobulin homology <IMM>
 F:355-372/Domain: transmembrane #status predicted <TM>
 F:373-416/Domain: intracellular #status predicted <INT>
 F:25/80/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 80.0%; Score 8; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONTARIG 9
 |||||||||

Db 24 ONTARIG 31

RESULT 4
 H64065
 mutator muth - Haemophilus influenzae (strain Rd KW20)
 N:Alternate names: DNA mismatch protein
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
 C:Accession: H64065
 R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
 R:Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman
 , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Georgagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; M0ID:95350630
 A:Accession: H64065
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-223 <TIGR>
 A:Cross-references: GB:U32723; GB:LA2023; NID:q1573363; PIDN:AA022062.1; PID:q1573374
 C:Genetics:
 A:Gene: muth
 C:Superfamily: mutator muth

Query Match 70.0%; Score 7; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
 |||||||||

Db 165 ITARIGE 171

RESULT 5
 Q08E43
 membrane antigen gp85 - human herpesvirus 4 (strain B95-8)
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
 C:Accession: F43044; A03787; S33040
 R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
 Mol. Biol. Med. 1, 21-45, 1983
 A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
 A:Reference number: A93065; M0ID:85057713
 A:Accession: F43044
 A:Molecule type: DNA
 A:Residues: 1-234 <BAN>
 A:Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24835.1; PID:q1334899

R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
 Nature 310, 207-211, 1984
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Reference number: A03794; MUID:84270667
 A:Contents: annotation; protein coding region
 C:Superfamily: Epstein-Barr virus membrane antigen gp85

Query Match 60.0%; Score 6; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 8.9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6
 |||||
 Db 108 AONITA 113

RESULT 6

H64181
 ABC-type transport system probable membrane spanning protein - Haemophilus influenzae (S
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Aug-1998
 C:Accession: H64181

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Feldman, J
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630
 A:Accession: H64181

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-238 <TIGR>
 A:Cross-references: GB:I42023; TIGR:H11079
 C:Superfamily: histidine permease protein M

Query Match 60.0%; Score 6; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6
 |||||
 Db 195 AONITA 200

RESULT 7

T51746
 RNA helicase RH17 [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
 C:Accession: T51746

R:Aubourg, S.; Kreis, M.; Lecharny, A.
 Nucleic Acids Res. 27, 628-636, 1999
 A:Title: The DEAD box RNA helicase family in Arabidopsis thaliana.
 A:Reference number: 222965; MUID:9862990

A:Accession: T51746
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <AUB>
 A:Cross-references: EMBL:AJ010468; PIDN:CAA09207.1
 C:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: RH17
 A:Map position: 2

Query Match 60.0%; Score 6; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10

Db 129 TARIGE 134
 |||||

RESULT 8
 S33667
 Probable integrase - Pseudomonas aeruginosa phage CTX

C:Species: Pseudomonas aeruginosa phage CTX
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
 C:Accession: S33667
 R:Hayashi, T.; Matsumoto, H.; Ohnishi, M.; Terawaki, Y.
 Mol. Microbiol. 7, 657-667, 1993
 A:Title: Molecular analysis of a cytotoxin-converting phage, phi-CTX, of Pseudomonas

A:Reference number: S33665; MUID:93225809
 A:Accession: S33667
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <HAY>
 A:Cross-references: EMBL:D13409; NID:q217776; PIDN:BA02675.1; PID:q217779
 C:Superfamily: hypothetical protein b1579

Query Match 60.0%; Score 6; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
 |||||
 Db 191 TARIGE 196

RESULT 9

T23984
 Hypothetical protein R06F6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23984

R:Chui, C.
 submitted to the EMBL Data Library, November 1994
 A:Reference number: Z19826
 A:Accession: T23984

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-429 <WIL>
 A:Cross-references: EMBL:Z46794; PIDN:CAA86783.1; GSPDB:GN00020; CESP:R06F6.4
 A:Experimental source: clone R06F6
 C:Genetics:
 A:Gene: CESP:R06F6.4
 A:Map position: 2
 A:introns: 68/3; 189/2; 228/3; 347/2

Query Match 60.0%; Score 6; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6
 |||||
 Db 345 AONITA 350

RESULT 10

H69133
 argininosuccinate lyase - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
 C:Accession: H69133

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
 K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A:Reference number: A69000; MUID:98037514

A:Accession: H69133
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-468 <MTH>
 A:Cross-references: GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84775.1; PID:g262131
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH269
 A:Start codon: TTG
 C:Superfamily: argininosuccinate lyase

Query Match 60.0%; Score 6; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 TARIGE 10
 Db 91 TARIGE 96

RESULT 11
 S30585
 hypothetical protein 5 - Methanobacterium thermoformicum
 C:Species: Methanobacterium thermoformicum
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Dec-1999
 C:Accession: S30585
 R:Noelling, J.; van Eden, F.J.M.; de Vos, W.M.
 submitted to the EMBL Data Library, November 1992
 A:Description: Distribution and characterization of plasmid-related sequence in the chrc
 A:Reference number: S30583
 A:Accession: S30585
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-471 <NOE>
 A:Cross-references: EMBL:X69114; NID:g44581; PIDN:CAA48867.1; PID:g44582
 C:Superfamily: Methanobacterium thermoformicum hypothetical protein 5

Query Match 60.0%; Score 6; DB 2; Length 471;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 NITARI 8
 Db 311 NITARI 316

RESULT 12
 T05671
 hypothetical protein F22113.200 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
 C:Accession: T05671
 R:Beyan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15420
 A:Accession: T05671
 A:Molecule type: DNA
 A:Residues: 1-548 <BEV>
 A:Cross-references: EMBL:AL035539
 A:Experimental source: cultivar Columbia; BAC clone F22113
 C:Genetics:
 A:Map position: 4
 A:Introns: 90/1; 129/1; 302/3; 420/3
 A>Note: F22113.200
 C:Superfamily: Arabidopsis thaliana hypothetical protein T7H20.60

Query Match 60.0%; Score 6; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8
 Db 440 NITARI 445

RESULT 13
 G84832
 ATP-dependent RNA helicase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84832
 R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MID:20083487
 A:Accession: G84832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-609 <STO>
 A:Cross-references: GB:AE002093; NID:g4895231; PIDN:AAD2817.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT9g40700
 A:Map position: 2

Query Match 60.0%; Score 6; DB 2; Length 609;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 TARIGE 10
 Db 440 TARIGE 445

RESULT 14
 E71733
 threonine--tRNA ligase (EC 6.1.1.3) - Rickettsia prowazekii
 N:Alternate names: threonyl-tRNA synthetase
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: E71733
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Slicheritz-Ponten, T.; Alsmark
 Nature 396, 133-140, 1998
 A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MID:99039499
 A:Accession: E71733
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-635 <AND>
 A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14684.1; PID:g386
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: thrs; RP221
 C:Function:
 A:Description: activates L-threonine and transfers it to the specific tRNA
 A:Pathway: protein biosynthesis
 A>Note: belongs to class-II synthetases
 C:Superfamily: threonine-tRNA ligase
 C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 60.0%; Score 6; DB 2; Length 635;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AQNITA 6
 Db 15 AQNITA 20

RESULT 15

I64045
recombination protein rec2 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: I64045
R:Flatschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geognagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64045
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-788 <TIGR>
A:Cross-references: GB:U32691; GB:I42023; NID:g1573004; PIDN:AAC21739.1; PID:g1573009; T
C:Genetics:
A:Gene: rec2

Query Match 60.0%; Score 6; DB 2; Length 788;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AONITA 6
|||||
DB 76 AONITA 81

Search completed: April 24, 2002, 09:23:17
Job time: 246 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:54 ; Search time 21.46 Seconds
(without alignments)

17.085 Million cell updates/sec

Title: US-09-689-469-6

Sequence: 1 AONTARIGE 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	100.0	404	1 RAGE_HUMAN	Q15109 homo sapien
2	90.0	402	1 RAGE_RAT	Q63495 ratus norv
3	90.0	403	1 RAGE_MOUSE	Q62151 mus musculu
4	80.0	416	1 RAGE_BOVIN	Q28173 bos taurus
5	70.0	223	1 MURH_HAIEIN	P44688 haemophilus
6	60.0	210	1 YA79_HAIEIN	P43023 haemophilus
7	60.0	234	1 PGP8_EBV	P03324 Epstein-barr
8	60.0	278	1 PROC_VIBAL	P52053 vibrio algi
9	60.0	401	1 ENO_THDAC	Q91411 thermoplasma
10	60.0	429	1 YRM4_CAEEL	Q09415 caenorhabdi
11	60.0	468	1 ARX_METTH	Q26369 methanobact
12	60.0	635	1 SYR_RICPR	O05347 rickettsia
13	60.0	788	1 REC2_HAIEIN	P44408 haemophilus
14	60.0	837	1 HFC1_HAIEIN	P33397 haemophilus
15	60.0	837	1 HFC2_HAIEIN	P45997 haemophilus
16	60.0	837	1 HFC3_HAIEIN	P45998 haemophilus
17	60.0	850	1 DEXT_STRMD	O54443 streptococc
18	60.0	125	1 BARM_HORVU	P28814 hordium vul
19	50.0	148	1 MYG_GALJA	P14398 galeorhinus
20	50.0	157	1 YI17_YEAST	P40502 saccharomyc
21	50.0	164	1 Y239_METUA	O57691 methanococc
22	50.0	164	1 YK00_YEAST	P36116 saccharomyc
23	50.0	166	1 RL10_UREPA	O9945 ureplasma
24	50.0	169	1 GBP_XENLA	O93343 xenopus lae
25	50.0	175	1 CRG2_XENLA	O91124 xenopus lae
26	50.0	180	1 TXLA_SYNY3	P73920 raphanus sa
27	50.0	183	1 DIN1_RAPSA	P30350 anas platyr
28	50.0	185	1 ADH_ANAPL	P37352 pseudomonas
29	50.0	204	1 LEXA_PSEAE	P71841 mycobacteri
30	50.0	224	1 PURO_MCTCO	O91841 mycobacteri
31	50.0	226	1 PURO_MCTCO	P29577 methanobact
32	50.0	227	1 YPVA_METTF	P29577 methanobact
33	50.0	241	1 MXIU_SHIFL	O06081 shigella fl

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	404 AA.
AC	Q15109; Q15279; Q9Y3R3; Q9H2X7;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).			
GN	AGER OR RAGE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Lung;			
RX	MEDLINE=92340547; PubMed=1378843;			
RA	Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,			
RA	Elliston K., Stern D., Shaw A.;			
RT	"Cloning and expression of a cell surface receptor for advanced			
RT	glycosylation end products of proteins.";			
RL	J. Biol. Chem. 267:14998-15004(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=95137587; PubMed=7835890;			
RA	Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,			
RA	Inoko H., Ikemura T.;			
RT	"Three genes in the human MHC class III region near the junction with			
RT	the class II: gene for receptor of advanced glycosylation end			
RT	products, PBX2 homeobox gene and a notch homolog, human counterpart			
RL	of mouse mammary tumor gene int-3.";			
RL	Genomics 23:408-419(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,			
RA	Banta A., Spies T., Hood L.;			
RT	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.			
RA	Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,			
RA	Yamamoto H.;			
RT	"Molecular heterogeneity of the receptor for advanced glycation			
RT	endproducts.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,			
RA	Schuler A., Huber G.;			
RT	"CDNA cloning of a novel secreted isoform of the human Receptor for			
RT	advanced Glycation End products (RAGE) and characterization of cells			
RT	co-expressing cell-surface scavenger receptors and Swedish mutant			
RT	amyloid precursor protein.";			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 1-12 FROM N.A.			

34	5	50.0	241	1	MXIU_SHISO	O52288 shigella so
35	5	50.0	241	1	RPPB_BRSLA	P33454 bovine resp
36	5	50.0	241	1	RPPB_HRSVA	P14156 human resp
37	5	50.0	241	1	RPPB_HRSV1	P24567 human resp
38	5	50.0	241	1	RPPB_HRSVA	P03421 human resp
39	5	50.0	241	1	RPPB_HRSV1	P12579 human resp
40	5	50.0	241	1	RPPB_ORSVW	O83956 ovine resp
41	5	50.0	261	1	DRBA_BACSU	P39071 bacillus su
42	5	50.0	262	1	FLUG_AGRTU	O44338 agrobacteri
43	5	50.0	264	1	LPXA_RICRI	P32199 rickettsia
44	5	50.0	288	1	CRTE_RHOSH	P54976 rhodobacter
45	5	50.0	291	1	AMPM_CHLPN	O92690 chlamydia p

RA	Hudson B.I., Futers T.S.: "Novel polymorphisms in the receptor for advanced glycation end-products (RAGE) gene.", EMBL/GenBank/DBJ databases.
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED RATE IN DIABETES.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/RAGESEC; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 2 C2-LIKE AND ONE V-LIKE DOMAINS.
CC	----- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
CC	-----
DR	EMBL; M91211; AAA03574.1; .
DR	EMBL; D28769; BAA05958.1; .
DR	EMBL; U089336; AAB47491.1; .
DR	EMBL; AB036432; BAA89369.1; .
DR	EMBL; AJ133822; CAB43108.1; .
DR	EMBL; AF208289; AAG35728.1; .
DR	MIM; 600214; .
DR	InterPro; IPRO003006; Ig_MHC.
DR	InterPro; IPRO003598; Ig_c2.
DR	InterPro; IPRO003600; Ig_like.
DR	Pfam; PF00047; Ig; 2.
DR	SMART; SM00408; IgC2; 1.
DR	SMART; SM00410; IG_Like; 1.
KW	PROSITE; PS00290; IG_MHC; 1.
KM	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
RK	Alternative splicing; Polymorphism.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFD
FT	DISULFD
FT	DISULFD
FT	CARBOHYD
FT	CARBOHYD
FT	DOMAIN
FT	VASPLIC
FT	VASPLIC
FT	VARIANT
FT	CONFLICT
FO	SEQUENCE

Query Match	100.0%	Score 10;	DB 1;	Length 404;
Best Local Similarity	100.0%	Pred. No. 0.00029;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

DB	23	MONITARI	32
RESULT	2		
AGE_RAT		STANDARD:	PRT: 402 AA.
AC	063495:		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).		
DE	AGER OR RAGE.		
OC	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE=Lung;		
RA	MEDLINE=97368045; PubMed=9224812;		
RA	Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,		
RA	Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;		
RT	"Recommendant advanced glycation end product receptor pharmacokinetics		
RL	in normal and diabetic rats.";		
RL	Mol. Pharmacol. 52:54-62(1997).		
CC	- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END		
CC	PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS		
CC	WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED		
CC	RATE IN DIABETES.		
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.		
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS		
CC	2 C2-LIKE AND ONE V-LIKE DOMAINS.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: L33413; AAA42027.1; -		
DR	InterPro: IPR003306; IG_MHC.		
DR	InterPro: IPR003598; IG_C2.		
DR	InterPro: IPR003600; IG_Like.		
DR	Pfam: PF00047; Ig_3.		
DR	SMART: SM00408; IGC2; 1.		
DR	SMART: SM00410; IG_Like; 1.		
DR	PROSITE: PS00290; IG_MHC; 1.		
KM	Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.		
FT	SIGNAL	1	22
FT	CHAIN	23	402
FT			
FT	DOMAIN	23	341
FT	DOMAIN	342	362
FT	DOMAIN	363	402
FT	DOMAIN	31	105
FT	DOMAIN	136	212
FT	DOMAIN	250	306
FT	DISULFID	38	98
FT	DISULFID	143	206
FT	DISULFID	257	299
FT	CARBOHYD	25	25
FT	CARBOHYD	80	80
SO	SEQUENCE	402 AA;	42663 MW;
			594481BC3A51E94E CXC64;

Query Match	90.0%;	Score 9;	DB 1;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 0.0037;		
Matches	9;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

AC P03224;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-DEC-1993 (Rel. 24, Last annotation update)
 DE PROBABLE MEMBRANE ANTIGEN GP85.
 GN BDLF3.
 OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
 CC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 CC NCBI_TaxID=10377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seglin C.,
 RA Tuffnell P.S., Barrell B.G.,
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."
 RL Nature 310:207-211(1984).
 CC -----
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 CC -----
 DR EMBL: V01555; CA24835.1; -
 DR PIR: A03787; Q0BE43.
 DR PIR: S33040; S33040.
 KW Membrane; Glycoprotein; Late protein.
 SO SEQUENCE 234 AA; 23791 MW; 48D6CED09331119E CRC64;

Query Match 60.0%; Score 6; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
 DB 108 AONITA 113

RESULT 8
 PROC_VIBAL STANDARD: PRT: 278 AA.
 ID PROC_VIBAL
 AC P52053;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
 GN PROC.
 OS Vibrio alginolyticus.
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 CC NCBI_TaxID=663;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=138-2;
 RX MEDLINE=97137009; PubMed=8962386;
 RX Nakamura T., Katoh Y., Shimizu Y., Matsuba Y., Umemoto T.;
 RT "Cloning and sequencing of novel genes from *Vibrio alginolyticus* that
 RT support the growth of K+ uptake-deficient mutant of *Escherichia*
 RT coli."
 RL Biochim. Biophys. Acta 1277:201-208(1996).
 CC -1- CATALYTIC ACTIVITY: L-PYRROLINE + NAD(P)(+) = L-PYRROLINE-5-
 CC CARBOXYLATE + NAD(P)H.
 CC -1- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: D50472; BAA09063.1; -
 DR InterPro: IPR000304; P5CR.
 DR Pfam: PF01089; P5CR; 1.
 DR PROSITE: PS00521; P5CR; 1.
 KW Oxidoreductase; Proline biosynthesis; NADP.
 SO SEQUENCE 278 AA; 29815 MW; 50359E5EF97CD68B CRC64;

Query Match 60.0%; Score 6; DB 1; Length 278;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
 DB 35 AONITA 40

RESULT 9
 ENO_THEAC STANDARD: PRT: 401 AA.
 ID ENO_THEAC
 AC Q9HJH1;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-
 DE GLYCERATE HYDRO-LYASE).
 GN ENO OR TA0882.
 OS Thermoplasma acidophilum.
 CC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
 CC Thermoplasma.
 CC NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermophilic scavenger *Thermoplasma*
 RT *acidophilum*."
 RL Nature 407:508-513(2000).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
 CC H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AL445065; CAC12011.1; -
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR Prodom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; FALSE NEG.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 146
 FT METAL 233
 FT METAL 274
 FT METAL 301
 SO SEQUENCE 401 AA; 43401 MW; 56D2C37CCA58AF02 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TARIG 9
 DB 288 TARIG 293

RESULT 10
 YRM4_CAEEL STANDARD; PRT; 429 AA.
 ID YRM4_CAEEL
 AC 009415; 009414;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 48.5 KDA PROTEIN R06F6.4 IN CHROMOSOME II.
 GN R06F6.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Poloderinae; Caenorhabditis.
 ON NCBI_TaxId=6239;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Chui C.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RC STRAIN-BRISTOL N2;
 RA Jones S.J.M.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PORENTIAL).
 CC -1- SIMILARITY: CONTAINS 1 MYND-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL: Z46794; CAAB6783.1; -
 DR WormBep: R06F6.4; CE16303.
 DR InterPro: IPR002893; Znf-MYND.
 DR Pfam: PF01753; Zf-MYND; 1.
 KW Hypothetical protein; Zinc-finger; DNA-binding; Nuclear protein.
 FT ZN_FING 26 64 MYND-TYPE.
 SO SEQUENCE 429 AA; 48546 MW; 51F223A6D0B56BA9 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AQNITA 6
 DB 345 AQNITA 350

RESULT 11
 ARLY_METTH STANDARD; PRT; 468 AA.
 ID ARLY_METTH
 AC 026369;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE) (ASAL).
 GN ARGH OR MTH269.
 OS Methanobacterium thermoautotrophicum.

OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacter.
 ON NCBI_TaxId=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RA MEDLINE=98037514; PubMed=93717463;
 RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
 RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nollig J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics."
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: L-ARGININOSUCCINATE = FUMARATE + L-ARGININE.
 CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE LYASE 1 FAMILY, ARGININOSUCCINATE LYASE
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AE000812; AAB84775.1; -
 DR InterPro: IPR000362; Fumarate_Lyase.
 DR Pfam: PF00206; Lyase_1; 1.
 DR PRINTS: PR00145; DCRYSTALLIN.
 DR PRINTS: PR00149; FUMARATELYASE.
 DR PROSITE: PS00163; FUMARATE_LYASES; FALSE_NEG.
 KW Arginine biosynthesis; Lyase; Complete proteome.
 SO SEQUENCE 468 AA; 52439 MW; 2DD1F7A65F5DF57 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10
 DB 91 TARIGE 96

RESULT 12
 SYT_RICPR STANDARD; PRT; 635 AA.
 ID SYT_RICPR
 AC 005947;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA LIGASE)
 DE (THRS).
 GN THRS OR RP221.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 ON NCBI_TaxId=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RX MEDLINE=97419517; PubMed=9274032;
 RA Andersson J.O., Andersson S.G.E.;
 RT "Genomic rearrangements during evolution of the obligate
 RT intracellular parasite Rickettsia prowazekii as inferred from an
 RT analysis of 52015 bp nucleotide sequence."
 RL Microbiology 143:2783-2795(1997).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RX MEDLINE=9039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Erilsson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-THREONINE + TRNA(THR) = AMP +
 CC PYROPHOSPHATE + L-THREONYL-TRNA(THR).
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y11780; CAA72469.1; -;
 DR EMBL: AJ235270; CAA14684.1; -;
 DR InterPro: IPR002106; AA.LRNL.Ligase_II.
 DR InterPro: IPR002314; TRNA-synt_2b.
 DR InterPro: IPR002320; TRNA-synt_thr.
 DR Pfam: PF00587; tRNA-synt_2b; 1.
 DR PRINTS: PRO1047; TRNASYNTHTHR.
 DR PROSITE: PS00179; AA-TRNA.LIGASE_II_1; FALSE_NEG.
 DR PROSITE: PS00339; AA-TRNA.LIGASE_II_2; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Zinc; Complete proteome.
 FT DOMAIN 242 533 CATALYTIC.
 FT METAL 333 333 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 384 384 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 510 510 ZINC (CATALYTIC) (BY SIMILARITY).
 SO SEQUENCE 635 AA; 72676 MW; B000D151A4F728D5 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 635;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
 DB 15 AONITA 20
 |||||
 |||||

RESULT 13
 RECD_HAEIN STANDARD; PRT; 788 AA.
 AC P44408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE RECOMBINATION PROTEIN 2.
 GN RECD OR REC-2 OR HI0061.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BC200;
 RX MEDLINE=94341577; PubMed=8063112;
 RA Clifton S.W., McCarthy D., Roe B.A.;
 RT "Sequence of the rec-2 locus of Haemophilus influenzae: homologues to
 RT comE-ORF3 of Bacillus subtilis and msdA of Escherichia coli";
 RL Gene 146:95-100(1994).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Guelin C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd";
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: MIGHT CONTRIBUTE TO TRANSFORMATION AS A MEMBER OF A
 CC MEMBRANE BOUND PORE COMPLEX AT THE BASE OF THE TRANSFORMASOME. IT
 CC COULD DIRECTLY INTERACT WITH TRANSFORMING DNA DURING TRANSLOCATION
 CC INDIRECTLY BY PARTICIPATING IN THE ASSEMBLY OF THE PORE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -1- SIMILARITY: TO B.SUBTILIS COMEC, N.GONORRHOEA COMA, AND E.COLI
 CC YCAL.
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 CC -----
 DR EMBL: L20805; AAC13733.1; -;
 DR EMBL: U32691; AAC21739.1; -;
 DR TIGR: H10061; -;
 DR InterPro: IPR001279; Beta_Lactam_mel.
 DR Pfam: PF00753; Lactamase_B; 1.
 KW Transport; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 3 23 POTENTIAL.
 FT TRANSMEM 27 47 POTENTIAL.
 FT TRANSMEM 51 71 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 FT TRANSMEM 313 333 POTENTIAL.
 FT TRANSMEM 367 387 POTENTIAL.
 FT TRANSMEM 401 421 POTENTIAL.
 FT TRANSMEM 434 454 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 508 528 POTENTIAL.
 FT CONFLICT 748 788 VENTAVSGGVAVNEFDRLFIQOARTKFSFWARVIGLSKE
 FT -> GRRYRCGASAGKFFSPRIPINPASPASKIIFLVCAQNMVI
 FT IKIGKIMRAIFTR (IN REF. 1).
 SO SEQUENCE 788 AA; 89355 MW; F31104595CB4E47A CRC64;

Query Match 60.0%; Score 6; DB 1; Length 788;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6
 DB 76 AONITA 81
 |||||
 |||||

RESULT 14
 HECL_HAEIN STANDARD; PRT; 837 AA.
 ID HECL_HAEIN
 AC P33397;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE OUTER MEMBRANE USHER PROTEIN HIFC PRECURSOR.
 GN HIFC.

```

OS Haemophilus influenzae.
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-EGAN / SEROTYPE B;
RX MEDLINE=94131580; PubMed=7905461;
RA Watson W.J., Gilsdorf J.R., Tucci M.A., McCrea K.W., Forney L.J.,
RA Mairs C.F.;
RT Identification of a gene essential for piliation in Haemophilus
RT influenzae type b with homology to the pilus assembly platform genes
RT of gram-negative bacteria.
RL Infect. Immun. 62:468-475(1994).
CC -1- FUNCTION: ESSENTIAL FOR PILATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-97 IS THE INITIATOR.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U02937; AAB53096.1; -
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher.1.
DR PROSITE: PS01151; FIMBRIAL_USHER.1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 837 OUTER MEMBRANE USHER PROTEIN HIFC.
FT DISULFID 813 833 POTENTIAL.
SQ SEQUENCE 837 AA; 92733 MW; BA529323AF63BF8B CRC64;

```

Query Match

Best Local Similarity 60.0%; Score 6; DB 1; Length 837;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10
 Db 253 TARIGE 258

```

RESULT 15
HFC2_HAEIN STANDARD; PRT; 837 AA.
AC P45957;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OUTER MEMBRANE USHER PROTEIN HIFC PRECURSOR.
GN HIFC.
OS Haemophilus influenzae.
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-AM30 (770235) / SEROTYPE B;
RX MEDLINE=95089703; PubMed=7997179;
RA van Ham M.S., van Alphen L., Mooi F.R., van Putten J.P.;
RT The fimbrial gene cluster of Haemophilus influenzae type b.
RL Mol. Microbiol. 13:673-684(1994).
CC -1- FUNCTION: ESSENTIAL FOR PILATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-97 IS THE INITIATOR.
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CC -----
DR EMBL: Z33502; CAA83902.1; -
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher.1.
DR PROSITE: PS01151; FIMBRIAL_USHER.1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 837 OUTER MEMBRANE USHER PROTEIN HIFC.
FT DISULFID 813 833 POTENTIAL.
SQ SEQUENCE 837 AA; 92641 MW; 0992A9F2C71F2774 CRC64;

```

Query Match

Best Local Similarity 60.0%; Score 6; DB 1; Length 837;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10
 Db 253 TARIGE 258

Search completed: April 24, 2002, 09:24:55
 Job time: 248 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:27 ; Search time 63.44 Seconds
(without alignments)
23.057 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 10
Sequence: 1 AQNITARIGE 10

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	342	4	Q9Y3R3	Q9Y3R3 homo sapien
2	90.0	402	11	Q35444	Q35444 mus musculu
3	60.0	32	6	Q9P8Q1	Q9P8Q1 bos taurus
4	60.0	127	12	Q9EAF5	Q9EAF5 human immun
5	60.0	298	10	Q9ZS04	Q9ZS04 arabidopsis
6	60.0	389	9	Q38644	Q38644 bacterioph
7	60.0	452	10	Q9LRM5	Q9LRM5 arabidopsis
8	60.0	471	1	Q04928	Q04928 methanobact
9	60.0	548	10	Q9SVR2	Q9SVR2 arabidopsis
10	60.0	609	10	Q9SHB9	Q9SHB9 arabidopsis
11	60.0	822	2	Q9L273	Q9L273 streptomyc
12	60.0	837	2	P94813	P94813 haemophilus
13	50.0	39	2	Q9RFA3	Q9RFA3 xenorhabdus
14	50.0	68	2	Q52235	Q52235 clostridium
15	50.0	71	4	Q9NPV6	Q9NPV6 homo sapien
16	50.0	72	11	Q9CZU1	Q9CZU1 mus musculu
17	50.0	72	11	Q9CR64	Q9CR64 mus musculu
18	50.0	74	5	Q9VWH8	Q9VWH8 dirosophila
19	50.0	77	4	Q9BZT4	Q9BZT4 homo sapien

20	5	50.0	90	12	Q98XX4	Q98XX4 human immun
21	5	50.0	91	12	Q9W063	Q9W063 human immun
22	5	50.0	98	12	Q91XR2	Q91XR2 human immun
23	5	50.0	99	12	Q992E8	Q992E8 human immun
24	5	50.0	99	12	Q98X93	Q98X93 human immun
25	5	50.0	111	4	Q9Y517	Q9Y517 homo sapien
26	5	50.0	114	10	Q9ARE8	Q9ARE8 lithosperm
27	5	50.0	118	2	Q9RVP1	Q9RVP1 deinococcus
28	5	50.0	120	10	Q9S0G4	Q9S0G4 tritlicum ae
29	5	50.0	120	10	Q9S0G3	Q9S0G3 tritlicum ae
30	5	50.0	125	2	Q9H2A1	Q9H2A1 pseudomonas
31	5	50.0	134	12	Q91HW2	Q91HW2 human immun
32	5	50.0	136	12	Q9E7L8	Q9E7L8 human cytom
33	5	50.0	137	10	Q9SMW1	Q9SMW1 arabidopsis
34	5	50.0	139	2	Q931A6	Q931A6 mycobacteri
35	5	50.0	142	2	Q9CK57	Q9CK57 pasteurella
36	5	50.0	142	2	Q9A2J7	Q9A2J7 caulobacter
37	5	50.0	143	10	Q9ZSL4	Q9ZSL4 chlororium i
38	5	50.0	146	10	P93180	P93180 hordeum vul
39	5	50.0	146	10	Q64392	Q64392 tritlicum ae
40	5	50.0	147	2	Q51542	Q51542 pseudomonas
41	5	50.0	147	2	Q9F3H0	Q9F3H0 streptomyc
42	5	50.0	148	10	Q64393	Q64393 tritlicum ae
43	5	50.0	152	12	Q41952	Q41952 murid herpe
44	5	50.0	157	1	Q9HR46	Q9HR46 halobacteri
45	5	50.0	160	2	Q9JN73	Q9JN73 streptomyc

ALIGNMENTS

RESULT 1
ID Q9Y3R3 PRELIMINARY: PRT: 342 AA.
AC Q9Y3R3;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
GN RAGESEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,
RT Schuler A., Huber G.;
RT "CDNA cloning of a novel secreted isoform of the human Receptor for
RT Advanced Glycation End products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant
RT amyloid precursor protein".
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ133822; CAB43108.1;
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR003600; Ig_Like.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig_2.
CC SMART: SM00408; Igc2: 1.
CC SMART: SM00410; Ig_Like; 1.
KW Signal; Receptor.
KW SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT 23 342 RECEPTOR FOR ADVANCED GLYCATION END
FT PRODUCTS.
SQ SEQUENCE 342 AA; 36193 MW; 35DDF66A1E39B38 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||
 DB 23 AONTARIGE 32

RESULT 2
 O35444
 ID O35444 PRELIMINARY; PRT; 402 AA.

AC O35444;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE RAGE.
 GN RAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;
 RL Submitted (OCR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF030001; AAB82007.1; -.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00408; IgC2; 1.
 DR SMART: SM00410; Ig_Like; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
 SO SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8C9902 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 QNTARIGE 10
 |||||
 DB 24 QNTARIGE 32

RESULT 3
 O9TR01
 ID O9TR01 PRELIMINARY; PRT; 32 AA.

AC O9TR01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92340546; PubMed=1321822;
 RA Schmidt A.M., Viana M., Gerlach M., Brett J., Ryan J., Kao J.,
 RA Esposito C., Hegarty H., Hurley W., Claus M.;
 RT Isolation and characterization of two binding proteins for advanced
 RT glycosylation end products from bovine lung which are present on the
 RT endothelial cell surface.;
 RL J. Biol. Chem. 267:14987-14997(1992).
 SO SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;

Query Match 60.0%; Score 6; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9
 |||||
 DB 4 ITARIG 9

RESULT 4
 O9EAJ5
 ID O9EAJ5 PRELIMINARY; PRT; 127 AA.

AC O9EAJ5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROTEASE (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=99-117635;
 RA Barlow K.L., Tatt I.D., Cane P.A., Pillay D., Clewley J.P.;
 RT "Detection of simple and complex recombinant strains of HIV-1 in the
 RT UK";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 DR EMBL: AJ296662; CAC03693.1; -.
 DR InterPro: IPR001969; Asp_protease.
 DR InterPro: IPR001995; Asp_prot_retrov.
 DR Pfam: PF00077; rvp; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; 1.
 DR PROSITE: PS50175; ASP_PROT_RETROV; 1.
 KM Aspartyl protease; Hydrolase.
 FT NON_TER 1 1
 SO SEQUENCE 127 AA; 13648 MW; CEAF72745863D5F4 CRC64;

Query Match 60.0%; Score 6; DB 12; Length 127;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9
 |||||
 DB 39 ITARIG 44

RESULT 5
 O9ZS04
 ID O9ZS04 PRELIMINARY; PRT; 298 AA.

AC O9ZS04;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE RNA HELICASE (FRAGMENT).
 GN RH17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA MEDLINE=99081866; PubMed=9862990;
 RA Aubourg S., Kreis M., Lecharny A.;
 RT "The DEAD box RNA helicase family in Arabidopsis thaliana";
 RL Nucleic Acids Res. 27:628-636(1999).
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 DR EMBL: AJ010468; CAA09207.1; -.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.

DR Pfam; PF00271; helicase-C; 1.
 DR SMART; SM00490; HelicC; 1.
 KW ATP-binding; Helicase.
 FT NON_TER 1
 SQ SEQUENCE 298 AA; 33973 MW; 6A38DF06CA2A7FAE CRC64;

Query Match 60.0%; Score 6; DB 10; Length 298;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
 |||||
 Db 129 TARIGE 134

RESULT 6
 O38644 PRELIMINARY; PRT; 389 AA.
 ID O38644; 038566;
 AC O38644; 038566; (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE PORE-FORMING CYTOTOXIN INTEGRASE.
 GN INT.
 OS bacteriophage phi CTX.
 OC Viruses.
 OX NCBI_TaxID=35343;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95124301; PubMed=7823914;
 RA Wang Z., Xiong G., Lutz F.;
 RT "Site-specific integration of the phage phi CTX genome into the
 RT Pseudomonas aeruginosa chromosome: characterization of the functional
 RT integrase gene located close to and upstream of atpP";
 RL Mol. Gen. Genet. 246:72-79(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hayashi T., Matsumoto H., Ohnishi M., Terawaki Y.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Laugewische F.W., Balzer A., Lutz F.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHICTX-C;
 RA Nakayama K., Hayashi T.;
 RT "Whole genome sequence of Pseudomonas aeruginosa cytotoxin-converting
 RT phage: phiCTX.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHICTX-C;
 RA Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
 RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene
 RT and the mechanism of activation of the protoxin.";
 RL Mol. Microbiol. 3:861-868(1989).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHICTX-C;
 RX MEDLINE=93225809; PubMed=8469112;
 RA Hayashi T., Matsumoto H., Ohnishi M., Terawaki Y.;
 RT "Molecular analysis of a cytotoxin-converting phage, phi CTX, of
 RT Pseudomonas aeruginosa: structure of the atpP-cotX region and
 RT integration into the serine tRNA gene.";
 RL Mol. Microbiol. 7:657-667(1993).
 DR EMBL; S75107; AAD14164.1; -
 DR EMBL; D13409; BA02675.1; -
 DR EMBL; S75107; AAD14165.1; -
 DR EMBL; Y13918; CAA74224.1; -
 DR EMBL; AB008550; BAA36272.1; -

DR InterPro; IPR002104; Phage_integrase.
 DR Pfam; PF00589; Phage_integrase; 1.
 SQ SEQUENCE 389 AA; 44431 MW; DA98223148071EFL CRC64;

Query Match 60.0%; Score 6; DB 9; Length 389;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10
 |||||
 Db 191 TARIGE 196

RESULT 7
 O9LRM5 PRELIMINARY; PRT; 452 AA.
 ID O9LRM5;
 AC O9LRM5;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE PECTATE LYASE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 DR EMBL; AB028621; BAB01365.1; -
 DR InterPro; IPR002022; Amb.allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PR00807; AMBALLENGEN.
 KW Lyase.
 SQ SEQUENCE 452 AA; 49985 MW; F31AD9097F923249 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 452;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTTAR 7
 |||||
 Db 87 QNTTAR 92

RESULT 8
 O04928 PRELIMINARY; PRT; 471 AA.
 ID O04928;
 AC O04928;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE HYPOTHEICAL 51.6 KDA PROTEIN (ORF5).
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 OX NCBI_TaxID=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93341463; PubMed=8393514;

RA Noelling J., Van Eden F.J.M., De Vos W.M.;
 RT "Distribution and characterization of plasmid-related sequences in the
 RT chromosomal DNA of different thermophilic *Methanobacterium* strains.";
 RL Mol. Gen. Genet. 240:81-91(1993).
 DR EMBL: X69114; CAA4867.1; -
 DR InterPro: IPR001434; DUF11.
 DR Pfam: PF01345; DUF11. 2.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51595 MW; 4AB8DB34FAB57BDE CRC64;

Query Match 60.0%; Score 6; DB 1; Length 471;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8
 DB 311 NITARI 316

RESULT 9
 O9SVE2 PRELIMINARY; PRT; 548 AA.
 AC O9SVE2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOHETICAL 60.8 KDA PROTEIN.
 GN F22113.200 OR AT4G38430.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL035539; CAB37499.1; -
 DR EMBL: AL161593; CAB80508.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 548 AA; 60847 MW; 7E6A8086E0FA5EC6 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 548;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8
 DB 440 NITARI 445

RESULT 10
 O9SHB9 PRELIMINARY; PRT; 609 AA.
 AC O9SHB9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ATP-DEPENDENT RNA HELICASE.
 GN ATG40700.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 DR EMBL: AC007660; AAD32817.1; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF002270; DEAD. 1.
 DR Pfam: PF002271; Helicase_C. 1.
 DR SMART: SM00487; DEXDC. 1.
 DR SMART: SM00490; HELIC. 1.
 KW ATP-binding; Helicase.
 SQ SEQUENCE 609 AA; 68213 MW; 0AB50FD42FE50DA0 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 609;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10
 DB 440 TARIGE 445

RESULT 11
 O9L273 PRELIMINARY; PRT; 822 AA.
 AC O9L273;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOHETICAL 91.7 KDA PROTEIN.
 GN SCL2.26C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL137778; CAB70938.1; -
KW Hypothetical protein.
SQ SEQUENCE 822 AA; 91739 MW; F210BCA05DA3C3E7 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9
DB 58 ITARIG 63

RESULT 12
ID P94813 PRELIMINARY; PRT; 837 AA.
AC P94813;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE USHER PROTEIN.
GN HAF.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F3031;
RX MEDLINE=97086624; PubMed=8932313;
RA Read T.D.; Dowdell M.; Satola S.W.; Farley M.M.;
RT "Duplication of pilus gene complexes of Haemophilus influenzae
RT biogroup aegyptius."
RL J. Bacteriol. 178:6564-6570(1996).
DR EMBL; U54780; AAB70873.1; -
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher.1.
DR PROSITE: PS01151; FIMBRIN_USHER.1.
SQ SEQUENCE 837 AA; 92683 MW; 6F0ED1D2FEC4176 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10
DB 253 TARIGE 258

RESULT 13
ID Q9RFA3 PRELIMINARY; PRT; 39 AA.
AC Q9RFA3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE MIAE (FRAGMENT).
GN MIAE.
OS xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus
OX NCBI_TaxID=628;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC19061;
RA Vivas E.I.; Goodrich-Blair H.;
RT "rpos is necessary for xenorhabdus nematophilus to colonize its
RT nematode host, Steinernema carpocapsae."
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF198628; AAF20817.1; -
FT NON_TER 1
SQ SEQUENCE 39 AA; 4465 MW; 910FCBEC87E9E4C CRC64;

Query Match 50.0%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITAR 7
DB 7 NITAR 11

RESULT 14
ID Q52235 PRELIMINARY; PRT; 68 AA.
AC Q52235;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PLASMID PNB2 (FROM CLOSTRIDIUM THERMOSACCHAROLYTICUM) REPN (FROM
DE CLOSTRIDIUM THERMOSACCHAROLYTICUM).
OS Clostridium thermosaccharolyticum (Thermoanaerobacterium
OS thermosaccharolyticum).
OX Plasmid PNB2.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacterium.
OX NCBI_TaxID=1517;
RN [1]
RP SEQUENCE FROM N.A.
RA Belogurova N.G.; Delver E.P.; Kalyuzhnyi S.V.; Varfolomeyev S.D.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; L38403; AAD12629.1; -
KW Plasmid.
SQ SEQUENCE 68 AA; 8115 MW; 36F4B9FDF9ED44FF CRC64;

Query Match 50.0%; Score 5; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARI 8
DB 35 ITARI 39

RESULT 15
ID Q9NPY6 PRELIMINARY; PRT; 71 AA.
AC Q9NPY6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE D6631M13.1 (SIMILAR TO MOUSE SEL1L (SEL-1 (SUPPRESSOR OF LIN-12,
DE C.ELEGANS)-LIKE)) (FRAGMENT).
GN D6631M13.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117333; CAC01943.1; -
FT NON_TER 71
SQ SEQUENCE 71 AA; 7756 MW; 3EF2C63469879DF4 CRC64;

Query Match 50.0%; Score 5; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2	QNTA	6						
Db	49	QNTA	53						

Search completed: April 24, 2002, 09:24:28
Job time: 252 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:37 ; Search time 66.28 Seconds
(without alignments)
11.176 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 48
Sequence: 1 AONTARIGE 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseqp/AA1981.DAT.*
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20: /SID8/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SID8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	20	AAV09353
2	48	100.0	10	21	AAV52135
3	48	100.0	15	18	AAW44208
4	48	100.0	15	18	AAW33762
5	48	100.0	16	18	AAW44214
6	48	100.0	16	18	AAW33768
7	48	100.0	30	20	AAV09349
8	48	100.0	30	21	AAV52134
9	48	100.0	318	18	AAW44200
10	48	100.0	318	18	AAW33754
11	48	100.0	332	21	AAV52130

12	48	100.0	340	18	AAW44199
13	48	100.0	340	18	AAW33753
14	48	100.0	404	22	AAW81925
15	44	91.7	30	20	AAV09350
16	44	91.7	30	20	AAV09351
17	40	83.3	30	20	AAV09352
18	33	68.8	30	18	AAW23337
19	33	68.8	420	21	AAV32428
20	32	66.7	269	16	AAW66289
21	32	66.7	269	16	AAW66293
22	32	66.7	269	18	AAW40807
23	32	66.7	269	18	AAW40808
24	32	66.7	269	20	AAV25522
25	32	66.7	772	19	AAW57632
26	32	66.7	1160	21	AAV52036
27	32	66.7	1160	21	AAV51665
28	32	66.7	1160	22	AAV51665
29	31	64.6	494	20	AAV34615
30	31	64.6	594	20	AAV45222
31	31	64.6	594	20	AAV39892
32	31	64.6	594	21	AAV95537
33	31	64.6	594	21	AAV96761
34	31	64.6	769	17	AAW03181
35	31	64.6	945	20	AAW88428
36	31	64.6	945	21	AAV69368
37	31	64.6	3722	12	AAV10145
38	30	62.5	79	22	AAW34806
39	30	62.5	260	21	AAV75595
40	30	62.5	272	22	AAV75595
41	30	62.5	315	17	AAW89323
42	30	62.5	315	17	AAW89322
43	30	62.5	317	22	AAW79601
44	30	62.5	328	20	AAV74117
45	30	62.5	420	21	AAV39434

ALIGNMENTS

RESULT 1	
ID AAV09353	standard; peptide; 10 AA.
XX	
XX AAV09353:	
XX	
DT 09-JUL-1999	(first entry)
XX	
XX	
DE Human RAGE V-domain peptide SEQ ID NO:5.	
KW RAGE, V-domain; receptor for advanced glycation endproduct;	
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;	
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;	
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;	
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;	
KW tumour; cancer; male impotence; wound healing; periodontal disease;	
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.	
XX	
OS Homo sapiens.	
XX	
PN W09918987-A1.	
XX	
PD 22-APR-1999.	
XX	
XX 09-OCT-1998:	98MO-US21346.
XX	
XX 09-OCT-1997:	97US-0948131.
XX	
PA (UYCO) UNIV COLUMBIA NEW YORK.	
XX	
PI Lamster I, Schmidt AM, Stern D, Yan SD;	
XX	
DR WPI; 1999-277439/23.	
XX	

PT New peptides based on an advanced glycation end product receptor are
 PT useful for treating Alzheimer's disease and Down's syndrome
 XX
 PS Claim 55; Page 85; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AONTARIGE 10
 |||||
 Db 1 agnitarige 10

RESULT 2

AA52135
 ID AAY52135 standard; peptide; 10 AA.

AC AAY52135;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #4.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 KM invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -
 XX
 PS Claim 30; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalises with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGE 10
 |||||
 Db 1 agnitarige 10

RESULT 3

AA44208
 ID AAW44208 standard; peptide; 15 AA.

AC AAW44208;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:12.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

KM AGE; antibody; vascular permeability; immunologically active fragment;
 KW diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody -
 PT Prevents receptor binding and therefore reduces vascular
 PT permeability, useful to treat diabetes mellitus
 XX
 PS Claim 2; Page 46; 90pp; English.

CC The present sequence represents an immunologically active fragment
 CC of a soluble human receptor to an advanced glycosylation end
 CC product (RAGE) polypeptide. The present invention describes

CC an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 15 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 1 agnitarige 10

RESULT 4
 AAW33762
 ID AAW33762 standard; peptide; 15 AA.

XX AAW33762;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 8.

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KM Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

XX 23-OCT-1997.

PD 11-APR-1997; 97WO-EP01832.

PF 16-APR-1996; 96US-0633147.

XX (SCHD) SCHERING AG.

PA Morser MJ, Nagashima M;

XX WPI: 1997-526458/48.

DR New soluble advanced glycosylation end-product receptor polypeptide

XX - used for reducing vascular permeability, complications of diabetes

PT etc., also for purification and to screen for modulators

XX Claim 6; Page 55; 91pp; English.

PS This is a peptide fragment of a human advanced glycosylation end-product
 CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active
 CC fragments or their mimetics can inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, atherosclerosis or
 CC retinopathy) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.

XX Sequence 15 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 1 agnitarige 10

RESULT 5
 AAW4214
 ID AAW4214 standard; peptide; 16 AA.

XX AAW4214;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.

XX Human: soluble receptor; advanced glycosylation end product; RAGE;
 KW AGE; antibody; vascular permeability; immunologically active fragment;
 KM diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

XX 23-OCT-1997.

PD 11-APR-1997; 97WO-EP01834.

PF 16-APR-1996; 96US-0633148.

XX (SCHD) SCHERING PATENTE AG.

PA Hollander DA, Morser MJ, Nagashima M;

XX WPI: 1997-558580/51.

DR Anti-advanced glycosylation end product polypeptide antibody -

XX prevents receptor binding and therefore reduces vascular

PT permeability, useful to treat diabetes mellitus

XX Claim 2; Page 49; 90pp; English.

PS The present sequence represents an immunologically active fragment
 CC of a soluble human receptor to an advanced glycosylation end
 CC product (RAGE) polypeptide. The present invention describes
 CC an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 16 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| | | | | | | | | |
Db 1 agnitariige 10

RESULT 6
AAW33768

ID AAW33768 standard; peptide; 16 AA.

AC AAW33768;

DE 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 14.

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
KW Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

PT New soluble advanced glycosylation end-product receptor polypeptide
PT - used for reducing vascular permeability; complications of diabetes
PT etc., also for purification and to screen for modulators

PS Disclosure; Page 9; 91pp; English.

CC This is a peptide fragment of a human advanced glycosylation end-product
CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active
CC fragments or their mimetics can inhibit interaction between advanced
CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
CC are used to treat diseases associated with AGE/RAGE interaction, such as
CC increased vascular permeability, diabetes mellitus (particularly
CC complications such as micro- or macro- vasculopathy or occlusive vascular
CC retinopathy) or haemodialysis-associated amyloidosis, also activation
CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
CC age-related disorders such as oxidative stress. These RAGE polypeptides
CC are also used, when immobilised, to purify AGE from a protein mixture and
CC to screen for compounds that are agonists and antagonists of AGE/RAGE
CC interaction. They can also be used diagnostically to detect abnormal
CC levels of AGE. Antibodies against RAGE polypeptides are useful as
CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
CC interaction between AGE and RAGE or other receptors and for purification
CC and quantification of RAGE polypeptides. The encoding nucleic acids are
CC used to express recombinant RAGE and as probes for isolating related
CC genes.

SO Sequence 16 AA;

Query Match 100.0%; Score 48; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 | | | | | | | | | |
1 agnitariige 10

RESULT 7

ID AAY09349 standard; peptide; 30 AA.

AC AAY09349;

DT 09-JUL-1999 (first entry)

DE Human RAGE V-domain peptide SEQ ID NO:1.

KW RAGE; V-domain; receptor for advanced glycation endproduct;
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
KW tumour; cancer; male impotence; wound healing; periodontal disease;
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

OS Homo sapiens.

PN WO9918987-A1.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US21346.

PR 09-OCT-1997; 97US-0948131.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are
PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an
CC amino acid sequence corresponding to an amino acid sequence of a
CC V-domain of a receptor for an advanced glycation end product (RAGE).
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
CC (ABP) interaction with a receptor for RAGE when the receptor is on the
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
CC extracellular assembly of an ABP into a fibril; (5) inhibiting
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
CC of a microglial cell into senile plaques; (7) inhibiting activation of a
CC microglial cell by an ABP; (8) treating a subject with a condition
CC associated with an interaction of an ABP with a receptor for RAGE on a
CC cell; (9) evaluating the ability of an agent to inhibit binding of an
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
CC inhibiting activation of a NP-kappaB gene in a cell; (11) inhibiting
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
CC with a receptor for RAGE when the receptor is on the surface of a cell;
CC and (13) treating a subject with a condition associated with an
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
CC can be used for treating conditions associated with an interaction of an
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
CC or neuronal degeneration.

SO Sequence 30 AA;

Query Match 100.0%; Score 48; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||
 Db 1 agnitarige 10

RESULT 8
 AAY52134
 ID AAY52134 standard; protein; 30 AA.

XX AAY52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;
 invasion; metastasis; amphoterin; neuron; inhibit; therapy.

XX Homo sapiens.

PN WO954485-A1.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

XX (UYCO) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

PT Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -

PS Claim 29; Page 62; 88pp; English.

XX This is the amino acid sequence of a fragment of the human soluble
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with
 CC a range of physiologically and pathophysiologically relevant ligands
 CC when considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.

XX Sequence 30 AA;

Query Match 100.0%; Score 48; DB 21; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||
 Db 1 agnitarige 10

RESULT 9

AAW44200
 ID AAW44200 standard; protein; 318 AA.

XX AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;
 KW AGE; antibody; vascular permeability; diabetes mellitus.

XX Homo sapiens.

FT Key location/Qualifiers

FT Misc-difference 66 /note="encoded by CCR"

XX WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

XX (SCHD) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

XX N-PADB; AAW12395.

PT Anti-advanced glycosylation end product polypeptide antibody -
 PT prevents receptor binding and therefore reduces vascular
 XX permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

XX The present sequence represents a mature human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in aging, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and it's
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 318 AA;

Query Match 100.0%; Score 48; DB 18; Length 318;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 |||||||||
 Db 1 agnitarige 10

RESULT 10
 ID AAW33754
 AAW33754 standard; protein; 318 AA.

XX AAW33754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KM Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9739121-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-EP01832.
 XX
 PR 16-APR-1996; 96US-0633147.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Morser MJ, Nagashima M;
 XX
 DR WPI; 1997-526458/48.
 XX
 DR N-PSDB; AAV06518.
 XX
 PT New soluble advanced glycosylation end-product receptor polypeptide
 PT - used for reducing vascular permeability, complications of diabetes
 PT etc., also for purification and to screen for modulators
 XX
 PS Claim 3; Fig 1B; 91pp; English.
 XX
 CC This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (318 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.
 XX
 SQ Sequence 318 AA;
 XX
 QY 1 AONTARIGE 10
 YQ |
 DB 1 agnitarige 10

Query Match 100.0%; Score 48; DB 18; Length 318;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 ID AAY52130 standard; protein; 332 AA.
 XX
 AC AAY52130;
 XX
 DT 28-JAN-2000 (first entry)
 XX
 DE Human Receptor to AGE (RAGE) amino acid sequence.
 XX
 KW Soluble receptor for advanced glycosylation endproducts; RAGE; tumour;
 KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.
 XX

XX Homo sapiens.
 OS
 XX
 PN WO9954485-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-US08427.
 XX
 PR 17-APR-1998; 98US-0062365.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Schmidt AM, Stern D;
 XX
 DR WPI; 2000-013260/01.
 XX
 PT Inhibiting tumour invasion or spreading by administration of soluble
 PT receptor for advanced glycation endproducts -
 XX
 PS Disclosure; Page 10-11; 88pp; English.
 XX
 CC This is the amino acid sequence of the human soluble Receptor for
 CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of
 CC physiologically and pathophysiologically relevant ligands when
 CC considering tumour invasion. In normal developing neurons RAGE
 CC colocalizes with amphoterin which is a matrix associated polypeptide.
 CC The expression of both RAGE and amphoterin decreases after birth, but
 CC both have increased expression in tumours. RAGE polypeptides
 CC AAY5132-Y52135 are used in the invention in a method for inhibiting
 CC tumour invasion and metastasis. The method involves inhibiting tumour
 CC invasion and metastasis via administration of a therapeutically effective
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.
 CC The invention also relates to a method for evaluating the ability of an
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE
 CC can be administered to a patient in a pharmaceutically acceptable
 CC carrier.
 XX
 SQ Sequence 332 AA;
 XX
 QY 1 AONTARIGE 10
 YQ |
 DB 1 agnitarige 10

Query Match 100.0%; Score 48; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ID AAW44199 standard; protein; 340 AA.
 XX
 AC AAW44199;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Human soluble receptor to an advanced glycosylation end product.
 XX
 KW Human; soluble receptor; advanced glycosylation end product; RAGE;
 KW AGE; antibody; vascular permeability; diabetes mellitus.
 XX
 OS Homo sapiens.
 XX
 PN WO9739125-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-EP01834.
 XX
 PR 16-APR-1996; 96US-0633148.
 XX

PA (SCHD) SCHERING PATENTE AG.
 XX
 PI Hollander DA, Morser MJ, Nagashima M;
 XX WPI: 1997-558580/51.
 DR N-PSDB: AAV12394.
 XX
 XX Anti-advanced glycosylation end product polypeptide antibody -
 PT prevents receptor binding and therefore reduces vascular
 PT permeability, useful to treat diabetes mellitus
 XX
 PS Claim 2; Page 40-41; 90pp; English.
 XX
 CC The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are
 CC non-enzymatically glycosylated proteins, which accumulate in vascular
 CC tissue in ageing, and at an accelerated rate in individuals with
 CC diabetes. The Ab, which prevents the interaction between an AGE and its
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for
 CC the isolation and purification of human RAGE polypeptide.
 CC
 SQ Sequence 340 AA:

Query Match 100.0%; Score 48; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10
 |||||||||
 Db 23 agnitarige 32

RESULT 13

AAM33753
 ID AAW33753 standard; Protein; 340 AA.

AC AAW33753;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;

KW Alzheimer's disease.

XX Homo sapiens.

XX WO9739121-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-EP01832.

XX 16-APR-1996; 96US-0633147.

XX (SCHD) SCHERING AG.

XX Morser MJ, Nagashima M;

XX WPI: 1997-526458/48.

XX N-PSDB: AAV06517.

XX New soluble advanced glycosylation end-product receptor polypeptide
 PT - used for reducing vascular permeability, complications of diabetes
 PT etc., also for purification and to screen for modulators
 XX

PS Claim 3; Fig 1A; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro-vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes.
 CC
 SQ Sequence 340 AA:

Query Match 100.0%; Score 48; DB 18; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10
 |||||||||
 Db 23 agnitarige 32

RESULT 14

AAB81925
 ID AAB81925 standard; protein; 404 AA.

AC AAB81925;

DT 15-JUN-2001 (first entry)

DE Extracorporeal circulation material receptor protein.

KW Extracorporeal circulation; carbonyl stress product; receptor;

KW diabetes; vascular lesion; excretory dysfunction.

XX Unidentified.

XX WO200118060-A1.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-JP06172.

XX 08-SEP-1999; 99JP-0254463.

XX (TORA) TORAY IND INC.

XX Shimizu S, Kubota M, Akiyama H, Usui M;

XX WPI: 2001-290314/30.

XX Material for extracorporeal circulation, applicable in selective
 PT elimination of diabetic complication factors such as carbonyl stress
 PT products caused by abnormally promoted carbonyl stress from excretory
 PT dysfunction in vascular lesions -
 XX

PS Claim 1; Page 31-32; 36pp; Japanese.

XX The present invention describes a material for extracorporeal circulation
 CC which is made from a water-insoluble carrier immobilized with a protein

CC having the sequence shown here. The materials of the invention, including
 CC adsorbents, are for extracorporeal circulation, which are applicable in
 CC the selective elimination of diabetic complication factors from a body
 CC fluid, and are therefore useful in treating vascular lesions like
 CC arteriosclerosis due to carbonyl stress products caused by abnormally
 CC promoted carbonyl stress from excretory dysfunction.

SO Sequence 404 AA;

Query Match 100.0%; Score 48; DB 22; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10
 Db 23 agnttarige 32

RESULT 15

AA09350
 ID AAY09350 standard; peptide; 30 AA.

XX AAY09350;

XX 09-JUL-1999 (first entry)

DE Mouse RAGE V-domain peptide SEQ ID NO:2.

XX RAGE; V-domain; receptor for advanced glycation endproduct;
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW tumour; cancer; male impotence; wound healing; periodontal disease;
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

XX Mus sp.

PN W09918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

XX MPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are
 useful for treating Alzheimer's disease and Down's syndrome

PS Claim 3: Page 78; 101pp: English.

XX The present invention describes novel isolated peptides (1) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting

CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.

SO Sequence 30 AA;

Query Match 91.7%; Score 44; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITFARIGE 10
 Db 2 qnltarige 10

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 Job time: 141 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:16 ; Search time 32.34 Seconds
(without alignments)
6.958 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 48
Sequence: 1 AONTIRAGE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents,AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfil1s1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	15	2	US-08-633-148-12	Sequence 12, Appl
2	48	100.0	16	2	US-08-633-148-18	Sequence 18, Appl
3	48	100.0	318	2	US-08-633-148-4	Sequence 4, Appl
4	48	100.0	340	2	US-08-633-148-2	Sequence 2, Appl
5	32	66.7	269	1	US-08-241-766-6	Sequence 6, Appl
6	32	66.7	269	1	US-08-241-766-7	Sequence 7, Appl
7	32	66.7	772	1	US-08-802-141-4	Sequence 4, Appl
8	31	64.6	769	3	US-08-434-000A-10	Sequence 10, Appl
9	31	64.6	769	3	US-09-312-157-10	Sequence 10, Appl
10	30	62.5	315	3	US-08-793-035-9	Sequence 9, Appl
11	30	62.5	315	3	US-08-793-035-10	Sequence 10, Appl
12	30	62.5	579	3	US-08-704-711A-1	Sequence 1, Appl
13	30	62.5	582	3	US-08-704-711A-2	Sequence 2, Appl
14	30	62.5	582	4	US-08-448-489-1	Sequence 1, Appl
15	30	62.5	582	4	US-09-211-704A-9	Sequence 9, Appl
16	29	60.4	198	1	US-08-278-091-16	Sequence 16, Appl
17	29	60.4	198	1	US-08-483-859-16	Sequence 16, Appl
18	29	60.4	198	1	US-08-472-173-16	Sequence 16, Appl
19	29	60.4	198	2	US-08-487-167-16	Sequence 16, Appl
20	29	60.4	198	2	US-08-482-816-16	Sequence 16, Appl
21	29	60.4	198	2	US-08-296-149-16	Sequence 16, Appl
22	29	60.4	198	2	US-08-801-499-16	Sequence 16, Appl
23	29	60.4	198	2	US-08-615-271-16	Sequence 16, Appl
24	29	60.4	198	3	US-09-074-660-16	Sequence 16, Appl
25	29	60.4	198	3	US-09-074-659-16	Sequence 16, Appl
26	29	60.4	198	3	US-09-106-468-16	Sequence 16, Appl
27	29	60.4	198	4	US-09-106-466A-16	Sequence 16, Appl

28	29	60.4	198	4	US-09-106-467-16	Sequence 16, Appl
29	29	60.4	394	3	US-08-673-814-6	Sequence 6, Appl
30	29	60.4	439	3	US-08-993-359-24	Sequence 24, Appl
31	29	60.4	439	3	US-09-221-654-2	Sequence 2, Appl
32	29	60.4	439	3	US-08-989-358A-2	Sequence 2, Appl
33	29	60.4	585	2	US-08-867-941-21	Sequence 21, Appl
34	29	60.4	585	2	US-09-074-658-21	Sequence 21, Appl
35	29	60.4	741	1	US-08-277-231A-4	Sequence 4, Appl
36	29	60.4	741	2	US-08-473-750-7	Sequence 7, Appl
37	29	60.4	741	2	US-08-477-326-7	Sequence 7, Appl
38	29	60.4	753	2	US-08-867-941-20	Sequence 20, Appl
39	29	60.4	753	4	US-09-074-658-20	Sequence 20, Appl
40	29	60.4	757	3	US-08-434-000A-6	Sequence 6, Appl
41	29	60.4	757	4	US-09-312-157-6	Sequence 6, Appl
42	29	60.4	771	3	US-08-434-000A-8	Sequence 8, Appl
43	29	60.4	771	4	US-09-312-157-8	Sequence 8, Appl
44	29	60.4	985	2	US-08-867-941-13	Sequence 13, Appl
45	29	60.4	985	2	US-08-867-941-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-633-148-12
; Sequence 12, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MORPHY ESO, MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-633-148-12

Query Match 100.0%; Score 48; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AONTIRAGE 10
|||||||

Db 1 AONITARIGE 10

RESULT 2

US-08-633-148-18

Sequence 18, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-18

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 3

US-08-633-148-4

Sequence 4, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-4

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 318;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 4

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 100.0%; Score 48; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
1111111111
DB 23 AONTARIGE 32

RESULT 5
US-08-241-766-6
Sequence 6, Application US/08241766
Patent No. 5686590

GENERAL INFORMATION:
APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: DELISLE, G. W.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241.766
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-766-6

Query Match 66.7%; Score 32; DB 1; Length 269;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
1111111111
DB 75 ADRITAIGE 84

RESULT 6
US-08-241-766-7

Sequence 7, Application US/08241766
Patent No. 5686590

GENERAL INFORMATION:
APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: DELISLE, G. W.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241.766
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-766-7

Query Match 66.7%; Score 32; DB 1; Length 269;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
1111111111
DB 75 ADRITAIGE 84

RESULT 7
US-08-802-141-4
Sequence 4, Application US/08802141
Patent No. 5773009

GENERAL INFORMATION:
APPLICANT: GLASS, ROGER I.
APPLICANT: GENTSCH, JOHN R.
APPLICANT: BHAN, M. K.
APPLICANT: DAS, BIMAL K.
TITLE OF INVENTION: ROTAVIRUS STRAIN AND RELATED
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,141
CLASSIFICATION: 424
FILING DATE: 19-FEB-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/231,041
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414,609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 688-9880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-802-141-4

Query Match
Best Local Similarity 66.7%; Score 32; DB 1; Length 772;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
:|:|:|
Db 31 ENTVOIGE 39

RESULT 8
US-08-434-000A-10
Sequence 10, Application US/08434000A
Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION DATA: including application
PRIORITY APPLICATION DATA: described below:
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: DESCRIPTION: Rat Polyimmunoglobulin Receptor
US-08-434-000A-10

Query Match
Best Local Similarity 64.6%; Score 31; DB 3; Length 769;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
:|:|:|
Db 470 QNTAVIGE 478

RESULT 9
US-09-312-157-10
Sequence 10, Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Rat Polyimmunoglobulin Receptor
US-09-312-157-10

Query Match 64.6%; Score 31; DB 4; Length 769;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
| | | | |
DB 470 ONATAVIGE 478

RESULT 10
US-08-793-035-9
; Sequence 9, Application US/08793035
; Patent No. 6011201

GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Pentem, Phillip A.
; TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-793-035-9

Query Match 62.5%; Score 30; DB 3; Length 315;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| : | : | : | : |
DB 256 ASDMTAKLGE 265

RESULT 11
US-08-793-035-10

; Sequence 10, Application US/08793035

; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Pentem, Phillip A.
; TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-793-035-10

Query Match 62.5%; Score 30; DB 3; Length 315;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| : | : | : | : |
DB 256 ASDMTAKLGE 265

RESULT 12
US-08-704-711A-1
; Sequence 1, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILD, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-1

Query Match 62.5%; Score 30; DB 3; Length 579;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
Db 126 QNTPKVGE 134

RESULT 13
US-08-704-711A-2
Sequence 2, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILK, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-2

Query Match 62.5%; Score 30; DB 3; Length 582;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
Db 129 QNTPKVGE 137

RESULT 14
US-08-448-489-1
Sequence 1, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 582
TYPE: PRT
ORGANISM: Homo sapiens
US-08-448-489-1

Query Match 62.5%; Score 30; DB 4; Length 582;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
Db 129 QNTPKVGE 137

RESULT 15
US-09-211-704A-9
Sequence 9, Application US/09211704A
Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: de Saint-Vis, Blandine Marie
APPLICANT: Fossiez, Francois
APPLICANT: Caux, Christophe
APPLICANT: Lebecque, Serge J.E.

;; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
;; TITLE OF INVENTION: and Methods
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DNAX Research Institute
;; STREET: 901 California Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/211,704A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/005,263
;; FILING DATE: 09-JAN-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ching, Edwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: SF0781K
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650)852-9196
;; TELEFAX: (650)496-1200
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 582 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-211-704A-9

Query Match 62.5%; Score 30; DB 4; Length 582;
Best Local Similarity 55.6%; Pred.No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 QNTARIGE 10
|||::||
DB 129 QNYTPKVE 137

Search completed: April 24, 2002, 09:18:16
Job time: 175 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:03 ; Search time 38.71 Seconds
(without alignments)
19.678 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 48
Sequence: 1 AONTARIGE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	404	1 T61596	advanced glycosyla
2	44	91.7	402	2 T09062	probable advanced
3	40	83.3	416	1 A42879	advanced glycosyla
4	36	75.0	879	2 E69792	conserved hypotet
5	35	72.9	547	2 T29567	hypothetical prote
6	34	70.8	391	2 B83203	arginate o-acetyl
7	34	70.8	808	2 E64492	hypothetical prote
8	34	70.8	1155	2 H71456	probable pyrolysin
9	34	70.8	1180	2 A35854	Integrin alpha-1 c
10	33	68.8	223	2 H64065	mutator muth - Hae
11	33	68.8	387	2 G84190	hypothetical prote
12	33	68.8	437	2 T64114	nfts protein homol
13	33	68.8	486	2 E42902	2-hydroxymucic s
14	33	68.8	550	2 T06379	SAR DNA-binding pr
15	33	68.8	560	2 T06377	SAR DNA-binding pr
16	33	68.8	792	2 B82752	penicillin binding
17	33	68.8	4436	2 E71086	hypothetical prote
18	32	66.7	435	2 T01805	hypothetical prote
19	32	66.7	439	2 T01807	hypothetical prote
20	32	66.7	468	2 H69133	argininosuccinate
21	32	66.7	508	2 T50180	nucleolar protein
22	32	66.7	625	2 T16777	hypothetical prote
23	32	66.7	772	2 A46110	outer capsid prote
24	32	66.7	941	2 F71332	probable chromosom
25	32	66.7	1160	1 DJEC3A	DNA-directed DNA p
26	32	66.7	1160	1 A45915	DNA-directed DNA p
27	32	66.7	1160	2 B85503	DNA polymerase III
28	32	66.7	1164	2 G82100	DNA polymerase III
29	32	66.7	1396	2 G70598	hypothetical prote

30	31	64.6	206	2 A64402	probable phosphati
31	31	64.6	215	2 JC5483	ABC-type transport
32	31	64.6	218	2 B83396	probable COA trans
33	31	64.6	240	2 E81261	probable ABC trans
34	31	64.6	250	2 C70869	hypothetical prote
35	31	64.6	262	2 T47002	hypothetical prote
36	31	64.6	268	2 D29826	hypothetical 28.8K
37	31	64.6	286	1 C35124	2,6-dioxo-6-phenyl
38	31	64.6	286	2 JN0816	2,6-dioxo-6-phenyl
39	31	64.6	318	2 E70117	membrane fusion pr
40	31	64.6	354	2 B47065	phosphate starvali
41	31	64.6	354	2 B85647	hypothetical prote
42	31	64.6	380	2 T04343	L-ascorbate oxidas
43	31	64.6	418	2 D75283	hypothetical prote
44	31	64.6	494	2 D64693	polymorphic outer
45	31	64.6	507	2 T20966	hypothetical prote

ALIGNMENTS

RESULT 1
161596
advanced glycosylation end-products receptor precursor - human
N:Alternate names: advanced glycosylation end product-binding protein, 35K, glycoprot
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: 161596; B42879; S27968
R:Snigaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.
Genomics 23, 408-419, 1994
A:Title: Three genes in the human MHC class III region near the junction with the cla
nterpart of mouse mammary tumor gene Int-3.
A:Reference number: A55562; MUID:95137587
A:Accession: 161596
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-404 <RES>
A:Cross-references: GB:D28769; NID:9561657; PTDN:BA05958.1; PTD:9561659
R:Neepser, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A:Reference number: A42879; MUID:92340547
A:Accession: B42879
A:Molecule type: mRNA
A:Residues: 'G', 2-99, 'R', 101-404 <NE>
A:Cross-references: EMBL:M91211; NID:9190845; PTDN:AAA03574.1; PTD:9190846
A:Experimental source: lung
A:Note: sequence extracted from NCBI backbone (NCBI:109438)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide
ases in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Genetics:
A:Gene: GDB:AGER
A:Cross-references: GDB:306354; OMIM:600214
A:Map position: 6p21.3-6p21.3
A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:23-404/Product: advanced glycosylation end products receptor #status predicted <EXT>
F:23-344/Domain: extracellular #status predicted <EXT>
F:31-101/Domain: immunoglobulin homology <IM1>
F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:345-363/Domain: transmembrane #status predicted <TM>
F:363-404/Domain: intracellular #status predicted <IM>
F:25-81/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

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Query Match      100.0%; Score 48; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANOTARIGE 10
    |||||||
Db 23 ANOTARIGE 32

RESULT 2
T09062
Probleb advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T09062
R:Rosen, L.; Mahairas, G.; Qin, S.; Ahern, M.E.; Bankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09062
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950
C:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31.100/Domain: immunoglobulin homology <IMM>

Query Match      91.7%; Score 44; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||||||
Db 24 ONITARIGE 32

RESULT 3
A42879
Advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: A42879; A42878; S27949
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A:Reference number: A42879; MUID:92340547
A:Molecule type: mRNA
A:Accession: A42879
A:Residues: 1-416 <NEER>
A:Cross-references: GB:M01212; NID:g163650; PID:AAA03575.1; PID:g163651
A:Experimental source: lung
A>Note: sequence extracted from NCBI backbone (NCBI:109436)
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
R:Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposto, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A>Title: Isolation and characterization of two binding proteins for advanced glycosylati
A:Reference number: A42878; MUID:92340546
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, 'X', '26-37', 'X', '39-49', 'XX', '52-54' <SCH>
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBI:109434)
C:Comment: Advanced glycosylation end-products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

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ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
A:Function:
A:Description: neuronal receptor for anaphroterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:1262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TM>
F:373-416/Domain: intracellular #status predicted <INT>
F:25.80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match      83.3%; Score 40; DB 1; Length 416;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||||||
Db 24 ONITARIGE 32

RESULT 4
E69792
Conserved hypothetical protein yeaA - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E69792
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Eutani, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Lardino
Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogikawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeder, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: E69792
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-879 <KUN>
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PID:CA012496.1; PID:g26329
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeaA

Query Match      75.0%; Score 36; DB 2; Length 879;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||||
Db 45 ONITARIGE 53

RESULT 5
T29567
Hypothetical protein C44C1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T29567

```


R:Bradshaw, H.; Stellyes, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C44C1.
 A:Reference number: Z20642
 A:Accession: T29567
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-547 <BRA>
 A:Cross-references: EMBL:U01030; PIDN:AA02364.1; CESP:C44C1.4
 C:Genetics:
 A:Gene: CESP:C44C1.4
 A:Introns: 31/3; 119/3; 178/2; 343/3; 373/3; 404/3; 440/2; 481/2; 531/2
 C:Superfamily: vacuolar protein sorting protein VPS45

Query Match 72.9%; Score 35; DB 2; Length 547;
 Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AONTARIGE 10
 |||||
 DB 265 ARNITANFGE 274

RESULT 6
 B83203
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: B83203
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AA06937.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: algJ; PA3549

Query Match 70.8%; Score 34; DB 2; Length 391;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AONTARIGE 10
 |||||
 DB 222 AONTATRIGE 231

RESULT 7
 E64492
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999
 A:Accession: E64492
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-808 <BOU>
 A:Cross-references: GB:U67595; GB:L77117; NID:g1592170; PIDN:AAB9570.1; PID:g1500434; T

C:Genetics:
 A:Map position: REV1521171-1518745

Query Match 70.8%; Score 34; DB 2; Length 808;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ONITARIGE 10
 :|||
 DB 229 ENITTRIGD 237

RESULT 8
 H71456
 A:Title: Probable pyrolysin (EC 3.4.-.-) homolog PH0310 [similarity] - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: H71456
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushtida, N.; Ogu
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137
 A:Accession: H71456
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1155 <KAN>
 A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29383.1; PID:g3256700
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by Genba
 C:Genetics:
 A:Gene: PH0310
 C:Keywords: hydrolase

Query Match 70.8%; Score 34; DB 2; Length 1155;
 Best Local Similarity 62.5%; Pred. No. 70;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 NITARIGE 10
 |||||
 DB 817 NITAKIGE 824

RESULT 9
 A35854
 A:Title: Integrin alpha-1 chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 20-Sep-1999
 C:Accession: A35854; S11243
 R:Ignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonet
 J. Cell Biol. 111, 709-720, 1990
 A:Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin
 A:Reference number: A35854; MUID:90338125
 A:Accession: A35854
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1180 <IGN>
 A:Cross-references: GB:X52140; NID:g56493; PIDN:CAA36384.1; PID:g56494
 C:Superfamily: unassigned collagens; von Willebrand factor type A repeat homology
 C:Keywords: cell adhesion; cytoskeleton; transmembrane protein
 F:170-345/Domain: von Willebrand factor type A repeat homology <WMA>

Query Match 70.8%; Score 34; DB 2; Length 1180;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ONITARIGE 9
 |||||
 DB 881 ONITCRVG 888

```

RESULT 10
H64065
mutator muth - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: DNA mismatch protein
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: H64065
R:Flischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: H64065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <TIGR>
A:Cross-references: GB:U32723; GB:I42023; NID:g1573363; PIDN:AAC22062.1; PID:g1573374; T
C:Genetics:
A:Gene: muth
C:Superfamily: mutator muth

Query Match
Best Local Similarity 68.8%; Score 33; DB 2; Length 223;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
DB 165 ITARIGE 171

RESULT 11
G84190
hypothetical protein Vng0310c [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84190
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leihnauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcic, Jung, K.H.; Alam, M.; Eitelas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A64160; MUID:20504483
A:Accession: G84190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <STO>
A:Cross-references: GB:AEO04437; NID:g10579939; PIDN:AGI8891.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0310C
C:Superfamily: conserved hypothetical protein MJ1249

Query Match
Best Local Similarity 68.8%; Score 33; DB 2; Length 387;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
DB 147 ONTARIGE 155

RESULT 12
I64114
nifs protein homolog H11295 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C:Accession: I64114; T09423
R:Flischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

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; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64114
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-437 <TIGR>
A:Cross-references: GB:U32809; GB:I42023; NID:g3212217; PIDN:AAC22941.1; PID:g1574753
R:White, O.; Clayton, R.A.; Kerlavage, A.R.; Flischmann, R.D.; Peterson, J.; Hickey, submitted to the EMBL Data Library, May 1998
A:Reference number: Z16667
A:Accession: T09423
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-437 <WHI>
A:Cross-references: EMBL:U32809; NID:g3212217; PID:g1574753
C:Genetics:
A:Gene: H11295
C:Superfamily: nifs protein

Query Match
Best Local Similarity 66.7%; Score 33; DB 2; Length 437;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
DB 385 ONTARIGE 393

RESULT 13
E42902
2-hydroxyxynuconic semialdehyde dehydrogenase (EC 1.2.1.-) - Pseudomonas putida plasmid
C:Species: Pseudomonas putida
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-May-2000
C:Accession: E42902; S18244; S23488
R:Harayama, S.; Reik, M.; Bairoch, A.; Neidle, E.L.; Ornston, L.N.
unpublished results 1991, cited by Genbank
A:Reference number: A57135
A:Accession: E42902
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-486 <HAR>
A:Cross-references: GB:M64747; NID:g151718; PIDN:AAA26053.1; PID:g151725
R:Harayama, S.; Reik, M.; Bairoch, A.; Neidle, E.L.; Ornston, L.N.
J. Bacteriol. 173, 7540-7548, 1991
A:Title: Potential DNA slippage structures acquired during evolutionary divergence of zolate dioxygenases.
A:Reference number: A41659; MUID:92041666
A:Contents: annotation
A:Note: Genbank cited this reference and reported DNA sequence with its translation n in the reference paper
R:Horn, J.M.; Harayama, S.; Timmis, K.N.
Mol. Microbiol. 5, 2459-2474, 1991
A:Title: DNA sequence determination of the TOL plasmid (pWMO) xylGR genes of Pseudom
A:Reference number: S18244; MUID:92167811
A:Accession: S18244
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-486 <HOR>
R:Neidle, E.L.; Hartnett, C.; Ornston, L.N.; Bairoch, A.; Reik, M.; Harayama, S.
Eur. J. Biochem. 204, 113-120, 1992
A:Title: Cis-diol dehydrogenases encoded by the TOL pWMO plasmid xylL gene and the Ac
A:Reference number: S23477; MUID:92155191
A:Accession: S23488
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-486 <NEI>
A:Cross-references: EMBL:M64747
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992

```

C:Genetics:
A:Gene: xyIG
A:Genome: plasmid TOL PWM0
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C:Keywords: oxidoreductase
F:42-308/Domain: aldehyde dehydrogenase homology <ALD>

Search completed: April 24, 2002, 09:19:04
Job time: 203 sec

Query Match 68.8%; Score 33; DB 2; Length 486;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| |||| ||
DB 74 ADGIFARFGE 83

RESULT 14
T06379
SAR DNA-binding protein 2 - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Jun-2000
C:Accession: T06379
R:Hatton, D.; Gray, J.C.
submitted to the EMBL Data Library, April 1998
A:Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to nucle
A:Reference number: 215637
A:Accession: T06379
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-550 <HAT>
A:Cross-References: EMBL:AF061963; NID:g3132697; PIDN:AMC16330.1; PID:g3132698
C:Genetics:
A:Gene: SARBP-2
C:Superfamily: garden pea SAR DNA-binding protein

Query Match 68.8%; Score 33; DB 2; Length 550;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| |||| ||
DB 281 APNLTAMVGE 290

RESULT 15
T06377
SAR DNA-binding protein-1 - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Jun-2000
C:Accession: T06377
R:Hatton, D.; Gray, J.C.
submitted to the EMBL Data Library, April 1998
A:Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to nucle
A:Reference number: 215637
A:Accession: T06377
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-560 <HAT>
A:Cross-References: EMBL:AF061962; NID:g3132695; PIDN:AMC16330.1; PID:g3132696
C:Genetics:
A:Gene: SARBP-1
C:Superfamily: garden pea SAR DNA-binding protein

Query Match 68.8%; Score 33; DB 2; Length 560;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONITARIGE 10
| |||| ||
DB 281 APNLTAMVGE 290

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:40 ; Search time 21.42 Seconds
(without alignments)
17.117 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 48
Sequence: 1 AONTARIGE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	404	1 RAGE_HUMAN	Q15109 homo sapien
2	44	91.7	402	1 RAGE_RAT	Q63495 rattus norv
3	44	91.7	403	1 RAGE_MOUSE	Q62151 mus musculu
4	40	83.3	416	1 RAGE_BOVIN	Q28173 bos taurus
5	34	70.8	1180	1 ITPL_RAT	P18614 rattus norv
6	33	68.8	223	1 MUTH_HAEN	P44688 haemophilus
7	33	68.8	270	1 NTFH_CLOCB	Q5270 clostridium
8	33	68.8	437	1 CSID_HAEN	Q57476 haemophilus
9	33	68.8	474	1 VDCC_STRD7	O95697 streptomyc
10	33	68.8	486	1 XYLG_PSEPU	P23105 pseudomonas
11	32	66.7	268	1 INHA_MYCAV	O07400 mycobacteri
12	32	66.7	269	1 INHA_MYCSM	P42829 mycobacteri
13	32	66.7	435	1 V413_ARATH	O04656 arabidopsis
14	32	66.7	439	1 V412_ARATH	O04658 arabidopsis
15	32	66.7	468	1 ARLY_METHN	O26369 methanobact
16	32	66.7	772	1 VP4_ROTHTU	O09113 human rotav
17	32	66.7	1159	1 DP3A_VITBCH	P52022 vibrio chol
18	32	66.7	1160	1 DP3A_ECOLI	P10443 escherichia
19	32	66.7	1160	1 DP3A_SALTY	P14567 salmonella
20	31	64.6	201	1 VID3_AGR6	P09816 agrobacteri
21	31	64.6	206	1 Y817_METJA	O58227 methanococc
22	31	64.6	286	1 BPMD_BURCE	P47229 burkholderi
23	31	64.6	354	1 PHOH_ECOLI	P31544 escherichia
24	31	64.6	767	1 CC10_SCHPO	P01129 schistosach
25	31	64.6	769	1 PIGR_RAT	P15083 rattus norv
26	31	64.6	1159	1 DP3A_PASMU	O96PK3 pasteurella
27	30	62.5	89	1 M7_LILHE	O40190 lilium henr
28	30	62.5	90	1 LML_LILLO	O43533 lilium long
29	30	62.5	90	1 LM2_LILLO	O43534 lilium long
30	30	62.5	115	1 YK03_CAEEL	P21110 caenorhabdi
31	30	62.5	137	1 K0GL_PSEDE	Q19945 pseudomonas
32	30	62.5	274	1 IF34_YEAST	O04067 saccharomyc
33	30	62.5	275	1 BLOI_PSEAE	O07293 pseudomonas

ALIGNMENTS

RESULT ID	RAGE_HUMAN	STANDARD	PRT	404 AA.
AC	015109: Q15279: Q9Y3R3; Q9H2X7;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).			
GN	AGER OR RAGE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Lung;			
RX	MEDLINE=92340547; PubMed=1378843;			
RA	Neepier M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,			
RA	Elliston K., Stern D., Shaw A.;			
RT	"Cloning and expression of a cell surface receptor for advanced			
RT	glycosylation end products of proteins.";			
RL	J. Biol. Chem. 267:14998-15004(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=95137587; PubMed=7835890;			
RA	Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,			
RA	Inoko H., Ikemura T.;			
RT	"Three genes in the human MHC class III region near the junction with			
RT	the class II: gene for receptor of advanced glycosylation end			
RT	products, PBX2 homeobox gene and a notch homolog, human counterpart			
RT	of mouse mammary tumor gene int-3.";			
RL	Genomics 23:408-419(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,			
RA	Banta A., Spies T., Hood L.;			
RT	Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.			
RA	Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,			
RA	Yamamoto H.;			
RT	"Molecular heterogeneity of the receptor for advanced glycation			
RT	endproducts.";			
RL	Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,			
RA	Schuler A., Huber G.;			
RT	"CDNA cloning of a novel secreted isoform of the human Receptor for			
RT	Advanced Glycation End products (RAGE) and characterization of cells			
RT	co-expressing cell-surface scavenger receptors and Swedish mutant			
RT	amyloid precursor protein.";			
RL	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 1-12 FROM N.A.			

34	30	62.5	285	1 YDHJ_ECOLI	P76185 escherichia
35	30	62.5	401	1 ENO_THBAC	Q9h1t1 thermoplasma
36	30	62.5	580	1 MM14_PIG	O9x490 sus scrofa
37	30	62.5	582	1 MM14_HUMAN	P50281 homo sapien
38	30	62.5	582	1 MM14_MOUSE	P53690 mus musculu
39	30	62.5	582	1 MM14_RABIT	O95220 oryctolagus
40	30	62.5	582	1 MM14_RAT	Q10739 rattus norv
41	30	62.5	772	1 VP4_ROTBB	P35746 bovine rota
42	30	62.5	850	1 DEXT_STRMU	O54443 streptococc
43	30	62.5	4644	1 DYHC_MOUSE	O9jhu4 mus musculu
44	30	62.5	4644	1 DYHC_RAT	P38650 rattus norv
45	29	60.4	83	1 RL23_HAALHA	Q06842 halobacteri

RA Hudson B.I., Puters T.S.;
 RT "Novel polymorphisms in the receptor for advanced glycation
 RL end-products (RAGE) gene";
 CC Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
 CC SECRETED (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/RAGESC;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
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 CC EMBL: M91211; AAA03574.1; -
 CC EMBL: D28769; BAA05958.1; -
 CC EMBL: U89336; BAA47491.1; -
 CC EMBL: AB036432; BAA69369.1; -
 CC EMBL: A1133823; CAB43108.1; -
 CC EMBL: AF208289; AAG35728.1; -
 CC MIM: 600214; -
 CC DR InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003598; IG_C2.
 CC DR InterPro: IPR003600; IG_Like.
 CC Pfam: PF00047; Ig_2.
 CC DR SMART: SM00408; Igc2; 1.
 CC DR SMART: SM00410; Ig_Like; 1.
 CC DR PROSITE: PS00290; IG_MHC; 1.
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
 CC Alternative splicing; Polymorphism.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 404
 CC FT DOMAIN 23 342
 CC FT TRANSMEM 343 363
 CC FT DOMAIN 364 404
 CC FT DOMAIN 31 106
 CC FT DOMAIN 137 214
 CC FT DOMAIN 252 308
 CC FT DISULFID 38 99
 CC FT DISULFID 144 208
 CC FT DISULFID 259 301
 CC FT CARBOHYD 25 25
 CC FT CARBOHYD 81 81
 CC FT DOMAIN 380 384
 CC FT VASPLIC 54 67
 CC FT VASPLIC 275 404
 CC FT VASPLIC 275 404
 CC FT VARIANT 100 100
 CC FT CONFLICT 1 1
 CC FT SEQUENCE 404 AA: 42802 MW: 0D584C436C30CE7 CRC64;
 CC
 CC Query Match 100.0%; Score 48; DB 1; Length 404;
 CC Best Local Similarity 100.0%; Pred. No. 0.013;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10

DB 23 AONTARIGE 32
 RESULT 2
 ID RAGE_RAT STANDARD; PRT; 402 AA.
 AC 063495;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunn E.,
 RA Worsler J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RL in normal and diabetic rats.";
 RL Mol. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: L33413; AAA42027.1; -
 CC InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003598; IG_C2.
 CC DR InterPro: IPR003600; IG_Like.
 CC Pfam: PF00047; Ig_3.
 CC DR SMART: SM00408; Igc2; 1.
 CC DR SMART: SM00410; Ig_Like; 1.
 CC DR PROSITE: PS00290; IG_MHC; 1.
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 402
 CC FT DOMAIN 23 341
 CC FT TRANSMEM 342 362
 CC FT DOMAIN 363 402
 CC FT DOMAIN 31 105
 CC FT DOMAIN 136 212
 CC FT DOMAIN 250 306
 CC FT DISULFID 38 98
 CC FT DISULFID 143 206
 CC FT DISULFID 257 299
 CC FT CARBOHYD 25 25
 CC FT CARBOHYD 80 80
 CC FT SEQUENCE 402 AA: 42663 MW: 594481BC3A51E94E CRC64;
 CC
 CC Query Match 91.7%; Score 44; DB 1; Length 402;
 CC Best Local Similarity 100.0%; Pred. No. 0.086;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
 |||||
 DB 24 QNTARIGE 32

RESULT 3
 RAGE_MOUSE STANDARD: PRT: 403 AA.
 ID RAGE_MOUSE
 AC 062151:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAUB/C; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Jungh E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 in normal and diabetic rats."
 RL Mol. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: L33412; AAA40040.1; -
 DR MGD; MGI:893592; Ager.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003598; Iq_C2.
 DR InterPro: IPR003600; Iq_Like.
 DR Pfam: PF00047; Iq_3.
 DR SMART; SM00408; Igc2; 1.
 DR SMART; SM00410; Iq_Like; 1.
 DR PROSITE; PS00290; Iq_MHC; 1.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 403
 FT FT
 FT DOMAIN 23 341
 FT TRANSMEM 342 362
 FT DOMAIN 363 403
 FT DOMAIN 31 105
 FT DOMAIN 136 213
 FT DOMAIN 251 307
 FT DISULFID 38 98
 FT DISULFID 143 207
 FT DISULFID 258 300
 FT CARBOHYD 25 25
 FT CARBOHYD 80 80
 FT SEQUENCE 403 AA: 42668 MW: 1279796FD1579357 CRC64;

Query Match 91.7%; Score 44; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGE 10
 |||||
 DB 24 QNTARIGE 32

RESULT 4
 RAGE_BOVIN STANDARD: PRT: 416 AA.
 ID RAGE_BOVIN
 AC Q28173;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
 GN AGER OR RAGE.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92340547; PubMed=1378843;
 RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
 RA Elliston K., Stern D., Shaw A.;
 RT "Cloning and expression of a cell surface receptor for advanced
 RT glycosylation end products of proteins."
 RL J. Biol. Chem. 267:14998-15004(1992).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: M91212; AAA03575.1; -
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003598; Iq_C2.
 DR InterPro: IPR003600; Iq_Like.
 DR Pfam: PF00047; Iq_2.
 DR SMART; SM00408; Igc2; 1.
 DR SMART; SM00410; Iq_Like; 1.
 DR PROSITE; PS00290; Iq_MHC; 1.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 416
 FT FT
 FT DOMAIN 23 352
 FT TRANSMEM 353 373
 FT DOMAIN 374 416
 FT DOMAIN 31 105
 FT DOMAIN 136 213
 FT DOMAIN 262 318
 FT DISULFID 38 98
 FT DISULFID 143 207
 FT DISULFID 269 311
 FT CARBOHYD 25 25
 FT CARBOHYD 80 80
 FT SEQUENCE N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

DE DNA MISMATCH REPAIR PROTEIN MUTH.
GN MUTH OR HI0403.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
RL Science 269:496-512(1995).
CC -I- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED
CC GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY
CC SIMILARITY).
CC -----
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CC -----
CC EMBL: U32723; AAC22062.1; -
CC DR HSSP: P06722; 2A2O.
CC DR TIGR: HI0403; -
CC KW DNA repair; Hydrolase; Endonuclease; Complete proteome.
CC SO SEQUENCE 223 AA; 24906 MW; 339A4EF9DA0E822A CRC64;

Query Match 68.8%; Score 33; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
| | | | | | |
Db 165 ITRIGE 171

RESULT 7
NIFH_CLOCB STANDARD; PRT; 270 AA.
AC Q59270;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NITROGENASE IRON PROTEIN (EC 1.18.6.1) (NITROGENASE COMPONENT II)
DE (NITROGENASE REDUCTASE).
GN NIFH.
OS Clostridium cellulosum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
CC Clostridium.
OX NCBI_TaxID=29355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 18532;
RA Chen T., Leschine S.B.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -I- CATALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 6 H(+) + N(ATP) =

CC 3 OXIDIZED FERREDOXIN + 2 NH(3) + N ADP + N ORTHOPHOSPHATE.
CC -I- COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.
CC CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC CC -I- SIMILARITY: BELONGS TO THE NIFH/CHL FAMILY.
CC CC -I- CAUTION: LACKS THE FIRST CONSERVED IRON-SULFUR BINDING CYSTEINE.
CC -----
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CC -----
CC EMBL: U59414; AAB63257.1; -
CC DR HSSP: P00459; INIP.
CC DR InterPro: IPR000392; NitrogenaseII.
CC DR Pfam: PF00142; fer4_NIFH; 1.
CC DR PRINTS: PR00091; NITROGENASEII.
CC DR PROSITE: PS00746; NIFH_FRXC_1; FALSE_NEG.
CC DR PROSITE: PS00692; NIFH_FRXC_2; 1.
CC KW Oxidoreductase; Nitrogen fixation; Iron-sulfur; 4Fe-4S; ATP-binding.
CC FT NP_BIND 8 15
CC FT METAL 128 128
CC FT SEQUENCE 270 AA; 29112 MW; 783335DBF0ADE88 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 270;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONITRIGE 10
| | : | : | : |
Db 19 ONITRIGE 27

RESULT 8
CSD_HAEIN STANDARD; PRT; 437 AA.
AC Q37476; O05054;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE CYSTEINE DESULFURASE (EC 4.4.1.-).
CC CSD OR HI1295.
CC OS Haemophilus influenzae.
CC OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
CC OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
RL Science 269:496-512(1995).
CC -I- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR AND SELENIUM
CC ATOMS FROM L-CYSTEINE, L-CYSTEINE, L-SELENOCYSTEINE, AND L-
CC SELENOCYSTINE TO PRODUCE L-ALANINE (BY SIMILARITY).
CC CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC CC -I- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES. CSD SUBFAMILY.
CC -----
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 CC -----
 CC EMBL; U32809; AAC22941.1; -
 CC TIGR; H11295; -
 CC InterPro: IPR000192; AminoTransf_class_V.
 CC Pfam: PF00266; aminotran_5; 1.
 CC PROSITE; PS00595; AA_TRANSFERR_CLASS_5; FALSE_NEG.
 CC KEGG; PYRIDOXAL PHOSPHATE; Complete proteome.
 CC BINDING 258 258 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC SEQUENCE 437 AA; 49048 MW; 1126FEC23DEBB9B CRC64;
 OY 2 ONTARIGE 10
 DB 385 ONTARIGE 393
 Query Match 68.8%; Score 33; DB 1; Length 437;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 9
 ID VDCG_STRD7 STANDARD; PRT; 474 AA.
 AC 09X697;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE VDCG PROTEIN.
 GN VDCG.
 OS Streptomyces sp. (strain D7).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=92742;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chow K.T., Pope M.K., Davies J.E.;
 RT "Characterization of a vanillic acid non-oxidative decarboxylation
 RT gene cluster from Streptomyces."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- INDUCTION: SYNTHESIZED IN RESPONSE TO VANILLATE.
 CC -1- SIMILARITY: BELONGS TO THE UBD FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF134589; AAD28782.1; -
 CC DR EMBL; AF134589; AAD28782.1; -
 CC DR InterPro: IPR002830; UPF0096.
 CC Pfam: PF01977; UPF0096; 1.
 CC SEQUENCE 474 AA; 52120 MW; 1DAE84542E75C75C CRC64;
 OY 1 AONTARIGE 10
 DB 35 AONTARIGE 44
 Query Match 68.8%; Score 33; DB 1; Length 474;
 Best Local Similarity 70.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 RESULT 10
 ID XYL6_PSEPO
 STANDARD; PRT; 486 AA.
 AC P23105;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE 2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.-) (HMSD).
 GN XYL6.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 CC NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92167811; PubMed=1791759;
 RA Horn J.M., Harayama S., Timmis K.N.;
 RT "DNA sequence determination of the TOL plasmid (pWMO) xylGJ genes of
 RT Pseudomonas putida: Implications for the evolution of aromatic
 RT catabolism.";
 RL Mol. Microbiol. 5:2459-2474(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=PAO;
 RX MEDLINE-92317087; PubMed=1339433;
 RA Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.;
 RT "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO
 RT encoding methylmalonate-semialdehyde dehydrogenase and 3-
 RT hydroxyisobutyrate dehydrogenase.";
 RL J. Biol. Chem. 267:13585-13592(1992).
 RN [3]
 RP SEQUENCE OF 1-15.
 RX MEDLINE-95173094; PubMed=7868591;
 RA Inoue J., Shaw J.P., Reik M., Harayama S.;
 RT "Overlapping substrate specificities of benzaldehyde dehydrogenase
 RT (the xylC gene product) and 2-hydroxymuconic semialdehyde
 RT dehydrogenase (the xylG gene product) encoded by TOL plasmid pWMO of
 RT Pseudomonas putida.";
 RL J. Bacteriol. 177:1196-1201(1995).
 CC -1- FUNCTION: 2-HYDROXYMUCONIC ACID SEMIALDEHYDE CAN BE CONVERTED TO
 CC 2-HYDROXYMUCONIC ACID SEMIALDEHYDE EITHER DIRECTLY BY THE ACTION OF 2-
 CC 2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (HMSH) OR BY THE ACTION OF
 CC THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD. CAN OXIDIZE
 CC NOT ONLY 2-HYDROXYMUCONIC SEMIALDEHYDE AND ITS ANALOGS BUT ALSO
 CC BENZALDEHYDE AND ITS ANALOGS. OPTIMAL PH OF CATALYSIS FOR THE
 CC OXIDATION OF 2-HYDROXYMUCONIC SEMIALDEHYDE AND BENZALDEHYDE ARE
 CC RESPECTIVELY 8.3 AND 9.6.
 CC -1- PATHWAY: META-CLEAVAGE PATHWAY FOR THE DEGRADATION OF PHENOLS,
 CC CRESOLS AND CATRECHOL. PHENOL METABOLISM.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
 CC -----
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 CC -----
 CC EMBL; M64747; AAA26053.1; -
 CC DR PIR; S18244; S18244.
 CC DR PIR; E42902; E42902.
 CC DR PIR; S23488; S23488.
 CC HSSP; P20000; 1A4Z.
 CC InterPro: IPR002086; Aldehyde_dehydr.
 CC Pfam: PF00171; aldehyd_1.
 CC PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 CC PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 CC Aromatic hydrocarbons catabolism: Oxidoreductase; NAD; Plasmid.
 FT ACT_SITE 254 254 BY SIMILARITY.
 FT ACT_SITE 288 288 BY SIMILARITY.
 FT CONFLICT 11 12 EL -> AF (IN REF. 3).
 FT SEQUENCE 486 AA; 51761 MW; 854303F121B2FFBD CRC64;

Query Match 68.8%; Score 33; DB 1; Length 486;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 74 ADGTRAFGE 83

RESULT 11
 INHA_MYCAV STANDARD: PRT; 268 AA.
 AC 007400:
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-DEPENDENT ENOYL-ACP REDUCTASE).
 GN INHA.
 OS Mycobacterium avium.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1764;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=GI10:
 RA MEDLINE=98195739; PubMed=9534249;
 RA Labo M., Gubserli L., de Rossi E., Speciale P., Riccardi G.;
 RT "Determination of a 15437 bp nucleotide sequence around the inhA gene of Mycobacterium avium and similarity analysis of the products of putative ORFs."
 RT Microbiology 144:807-814 (1998).
 RL
 CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS. THIS ISOZYME IS INVOLVED IN MYCOLIC ACID BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC
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 CC -----
 CC DR EMBL: AF002133; AAC46204.1;..
 CC KM Oxidoreductase; NAD: Fatty acid biosynthesis.
 CC FT NP_BIND 135 164 NAD (POTENTIAL).
 CC SQ SEQUENCE 268 AA; 28529 MW; F73501BD2B0F9990 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 268;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 75 AORVTGEIGE 84

RESULT 12
 INHA_MYCSM STANDARD: PRT; 269 AA.
 AC P42829:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-

DEPENDENT ENOYL-ACP REDUCTASE).
 GN INHA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 700084 / MC(2)155;
 RA MEDLINE=94112548; PubMed=8284673;
 RA Banerjee A., Dubnau E., Quemard A., Balasubramanian V., Um K.S., Wilson T., Collins D., de Lisle G., Jacobs W.R. Jr.;
 RT "inhA, a gene encoding a target for isoniazid and ethionamide in Mycobacterium tuberculosis.";
 RT Science 263:227-230 (1994).
 RL
 CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS. THIS ISOZYME IS INVOLVED IN MYCOLIC ACID BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: INVOLVED IN THE RESISTANCE AGAINST THE ANTITUBERCULOSIS DRUGS ISONIAZID AND ETHIONAMIDE.
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC
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 CC -----
 CC DR EMBL: U02530; AAC43211.1;..
 CC DR HSSP: P46533; 1ENZ.
 CC KM Oxidoreductase; NAD: Fatty acid biosynthesis; Antibiotic resistance.
 CC FT NP_BIND 136 165 NAD (POTENTIAL).
 CC FT VARIANT 94 94 S -> A (IN INH-RESISTANT STRAIN MC SQUARED 651).
 CC SQ SEQUENCE 269 AA; 28527 MW; AD3BD962DB78FC6 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 269;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 75 ADRTAFGE 84

RESULT 13
 Y413_ARATH STANDARD: PRT; 435 AA.
 AC O04656:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 48.8 KDA PROTEIN M021B04.13.
 GN A_TW021B04.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Dante M., Mansley P., Gibson A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
 CC
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 CC -----
 DR EMBL: AF007271; AAB61074.1; -
 DR InterPro: IPR002687; Nop.
 DR Pfam: PF01798; Nop; 1.
 DR ProDom: PD004104; Nop; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 435 AA; 48818 MW; BE502C8C244AF085 CRC64;

Query Match
 Best Local Similarity 66.7%; Score 32; DB 1; Length 435;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 238 APTLTALVGE 247

RESULT 14
 ID Y412.ARATH STANDARD; PRT; 439 AA.
 AC 004658;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 GN HYPOTHETICAL 47.9 KDA PROTEIN M021B04.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=CV. COLUMBIA;
 RA Dancie M., Wamsley P., Gibson A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF007271; AAB61073.1; -
 DR InterPro: IPR002687; Nop.
 DR Pfam: PF01798; Nop; 1.
 DR ProDom: PD004104; Nop; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 439 AA; 47932 MW; BE0E2214F9BCAFDB CRC64;

Query Match
 Best Local Similarity 66.7%; Score 32; DB 1; Length 439;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 281 APTLTALVGE 290

RESULT 15
 ARLY_METTH STANDARD; PRT; 468 AA.
 ID ARLY_METTH

AC 026369;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-ANG-2001 (Rel. 40, Last annotation update)
 DE ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE) (ASAL).
 GN ARGH OR MTH269.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacter.
 OX NCBI_TaxID=145262;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: L-ARGININOSUCCINATE = FUMARATE + L-ARGININE.
 CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE LYASE I FAMILY. ARGININOSUCCINATE LYASE
 CC SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE00812; AAB84775.1; -
 DR InterPro: IPR000362; Fumarate_Lyase.
 DR Pfam: PF00206; Lyase_1; 1
 DR PRINTS; PR00145; DCRISTALLIN.
 DR PRINTS; PR00145; FUMARATE_LYASE.
 DR PROSITE; PS00163; FUMARATE_LYASES; FALSE_NEG.
 KW Arginine biosynthesis; Lyase; Complete proteome.
 SQ SEQUENCE 468 AA; 52439 MW; 2DD1F7A65F5D57 CRC64;

Query Match
 Best Local Similarity 85.7%; Score 32; DB 1; Length 468;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
 DB 90 VTARIGE 96

Search completed: April 24, 2002, 09:20:41
 Job time: 255 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:13 ; Search time 62.94 Seconds
(without alignments)
23.240 Million cell updates/sec

Title: US-09-689-469-6
Perfect score: 48
Sequence: 1 AONITRARGE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mammal:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	342	4	O9Y3R3
2	44	91.7	402	11	O35444
3	37	77.1	246	2	P71291
4	36	75.0	879	2	O30579
5	36	75.0	879	2	O31504
6	35	72.9	84	12	O40496
7	35	72.9	547	5	O18609
8	35	72.9	851	12	O73304
9	34	70.8	76	12	O9WAE2
10	34	70.8	90	12	O76444
11	34	70.8	90	12	O9YWS9
12	34	70.8	391	2	O51393
13	34	70.8	401	2	O9ZIC1
14	34	70.8	459	12	O91900
15	34	70.8	715	2	O30965
16	34	70.8	808	1	O58937
17	34	70.8	1155	1	O58048
18	33	68.8	32	6	O9TRQ1
19	33	68.8	42	10	O9LE26

20	33	68.8	135	2	O56486	O56486 unidentified
21	33	68.8	135	2	O56487	O56487 unidentified
22	33	68.8	135	2	O56489	O56489 unidentified
23	33	68.8	141	2	O66292	O66292 unidentified
24	33	68.8	141	2	O66293	O66293 unidentified
25	33	68.8	141	2	O66324	O66324 unidentified
26	33	68.8	141	2	O66349	O66349 unidentified
27	33	68.8	141	2	O66358	O66358 unidentified
28	33	68.8	141	2	O66361	O66361 unidentified
29	33	68.8	141	2	O66499	O66499 unidentified
30	33	68.8	269	2	O9CBM1	O9CBM1 mycobacteri
31	33	68.8	387	1	O9HSB6	O9HSB6 halobacteri
32	33	68.8	550	10	O65335	O65335 pismu saliv
33	33	68.8	555	2	O9A310	O9A310 caulobacter
34	33	68.8	560	10	O65334	O65334 pismu saliv
35	33	68.8	792	2	O9PEZ4	O9PEZ4 xyella fas
36	33	68.8	848	5	O25198	O25198 hydra atten
37	33	68.8	4436	1	O58659	O58659 pyrococcus
38	32	66.7	42	10	O9LE27	O9LE27 lycopodium
39	32	66.7	42	10	O9LDB7	O9LDB7 marichantia
40	32	66.7	149	2	O9F6U7	O9F6U7 bacteroides
41	32	66.7	223	2	O9S6L2	O9S6L2 corynebacte
42	32	66.7	247	2	O9AQM1	O9AQM1 pseudomonas
43	32	66.7	268	2	O9Z473	O9Z473 corynebacte
44	32	66.7	269	2	O9X6U5	O9X6U5 brevbacter
45	32	66.7	269	2	O9LAH3	O9LAH3 corynebacte

ALIGNMENTS

RESULT 1
O9Y3R3 PRELIMINARY; PRT; 342 AA.

AC O9Y3R3: 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
GN RAGESEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Malherbe P., Richards J., Gallard H., Thompson A., Diener C.,
RA Schuler A., Huber G.;
RT "CDNA cloning of a novel secreted isoform of the human Receptor for
RT co-expressing cell-surface scavenger receptors and Swedish mutant
RT amyloid precursor protein.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: A113822; CABA3108.1;
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SMO0408; IGC2; 1.
DR SMART: SMO0410; IG_Like; 1.
KW Signal; Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 342 RECEPTOR FOR ADVANCED GLYCATION END
FT PRODUCT.
SQ SEQUENCE 342 AA; 36193 MW; 35DDF6A13E3B38 CRC64;

Query Match 100.0%; Score 48; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANONTARIGE 10
 DB 23 ANONTARIGE 32

RESULT 2
 ID 035444 PRELIMINARY; PRT: 402 AA.
 AC 035444;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PAGE.
 GN PAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Lorentz C., Schmidt S., Tipton S., Traicoff R., Zachrone K., Hood L.;
 RL Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 CC EMBL; AF030001; AAB82007.1; -
 DR InterPro; IPR003598; Iq_C2.
 DR InterPro; IPR003600; Iq_Like.
 DR InterPro; IPR003006; Iq_MHC.
 DR Pfam; PF00047; Iq_3.
 DR SMART; SM00408; IqC2; 1.
 DR SMART; SM00410; Iq_Like; 1.
 DR PROSITE; PS00290; Iq_MHC; UNKNOWN_1.
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 91.7%; Score 44; DB 11; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
 DB 24 ONTARIGE 32

RESULT 3
 ID P71291 PRELIMINARY; PRT: 246 AA.
 AC P71291;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-FEB-1997 (TREMBLrel. 02, Last annotation update)
 DE SIMILAR TO E. COLI YJHH.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schumm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
 RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
 RA Laskhari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
 RA Davis R.W.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U70214; AAB08689.1; -
 SQ SEQUENCE 246 AA; 26806 MW; 93FBCA6B432BE37D CRC64;

Query Match 77.1%; Score 37; DB 2; Length 246;
 Best Local Similarity 70.0%; Pred. No. 8.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANONTARIGE 10

DB 78 ADMNARIGE 87

RESULT 4
 ID 030579 PRELIMINARY; PRT: 879 AA.
 AC 030579;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE YEBA.
 GN YEBA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 TRPC2;
 RA Borris R., Schroeter R.;
 RL Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF01532; AAB66474.1; -
 DR InterPro; IPR002052; N6_Mtase.
 DR PROSITE; PS00092; N6_Mtase; UNKNOWN_1.
 SQ SEQUENCE 879 AA; 101108 MW; B5E35926796B49AA CRC64;

Query Match 75.0%; Score 36; DB 2; Length 879;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
 DB 45 ONLTRKIGE 53

RESULT 5
 ID 031504 PRELIMINARY; PRT: 879 AA.
 AC 031504;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE YEBA PROTEIN.
 GN YEBA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertoro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borris R., Bourrier L., Brans A., Braun M., Brigelli S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Dentan F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D.,
 RA Frits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Ilaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Portetelle S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni K.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Wetzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z99107; CAB12496.1; -;
 DR InterPro: IPR002052; N6_Mtase.
 DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 879 AA; 101157 MW; 555B1607264285A5 CRC64;

Query Match 75.0%; Score 36; DB 2; Length 879;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGE 10
 DB 45 QNTLRVGE 53

RESULT 6
 ID 040496 PRELIMINARY; PRT; 84 AA.
 AC 040496;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-95M145;
 RA Peeters M., Koumare B., Mulanga C., Brengues C., Mountrou B.,
 RA Bougoudogo F., Ravel S., Bibollet-Ruche F.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y14356; CAI74727.1; -;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 84
 FT NON_TER 84
 SQ SEQUENCE 84 AA; 9256 MW; 6D5031F860B23C75 CRC64;

Query Match 72.9%; Score 35; DB 12; Length 84;
 Best Local Similarity 55.6%; Pred. No. 6.8;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGE 10
 DB 65 QNTAKLQ 73

RESULT 7
 ID 018609 PRELIMINARY; PRT; 547 AA.
 AC 018609;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO YEAST VACUOLAR SORTING PROTEIN SLP1.
 GN 44C1.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showken R.,
 RA Smaiden N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wainstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bradshaw H., Stellyes L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41030; AAA82364.1; -;
 DR InterPro: IPR001619; Sec1.
 DR Pfam: PF00995; Sec1; 1.
 SQ SEQUENCE 547 AA; 62119 MW; 4F8B7B99607789E1 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 547;
 Best Local Similarity 70.0%; Pred. No. 55;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10
 DB 265 ARNTANFGE 274

RESULT 8
 ID 073304 PRELIMINARY; PRT; 851 AA.
 AC 073304;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96263682; PubMed=8924250;
 RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J.,
 RA Daniels R.S.;
 RT "An efficient method for the rescue and analysis of functional HIV-1
 RT splice site.";
 RL AIDS 10:39-46(1996).
 DR EMBL: U36879; AAC55538.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.
 KW Envelope protein.
 SQ SEQUENCE 851 AA; 96525 MW; F985DB4E881F718 CRC64;

Query Match 72.9%; Score 35; DB 12; Length 851;
 Best Local Similarity 87.5%; Pred. No. 90;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NITRARGE 10
 ||:|:|:
 Db 157 NITRIGE 164

RESULT 9
 O9WBE2 PRELIMINARY; PRT; 76 AA.

AC O9WBE2; 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE GP120 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Bobkov A.F., Kazemova E.V., Selimova L.M., Ladnaya N.N.,
 Kravchenko A.V., Foley B., Morrison I., Pokrovsky V.V.,
 Chelingsong-Popov R., Weber J.N.;
 RT "HIV-1 gagD/envG recombinants in Russia."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF051468; AAD02595.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 FT NON_TER 1 76
 FT NON_TER 1 76
 SQ SEQUENCE 76 AA; 8205 MW; 3B731642912E1954 CRC64;

Query Match 70.8%; Score 34; DB 12; Length 76;
 Best Local Similarity 55.6%; Pred. No. 9.9;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
 ||:|:|:
 Db 47 QNVTTRIGE 55

RESULT 10
 O76444 PRELIMINARY; PRT; 90 AA.

AC O76444; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ENVELOPE GLYCOPROTEIN 120 V3 REGION (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Lukashov V.V., Cornelissen M.T., Goudsmit J., Papushvili M.N.,
 Rytlik P.G., Khalitov R.M., Karamov E.V., De Wolf F.;
 RT "Simultaneous introduction of distinct HIV-1 subtypes into different
 risk groups in Russia, Byelorussia and Lithuania."
 RL AIDS 9:435-439(1995).
 DR EMBL: U38413; AAA91757.1; -.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 1 90
 FT NON_TER 1 90
 SQ SEQUENCE 90 AA; 10076 MW; 5AD80C9ADB28E330 CRC64;

Query Match 70.8%; Score 34; DB 12; Length 90;
 Best Local Similarity 55.6%; Pred. No. 12;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGE 10
 ||:|:|:
 Db 73 QNVTTRIGE 81

RESULT 11
 O9YWS9 PRELIMINARY; PRT; 90 AA.

AC O9YWS9; 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE GP120 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Bobkov A.F., Kazemova E.V., Selimova L.M., Ladnaya N.N.,
 Kravchenko A.V., Foley B., Morrison I., Pokrovsky V.V.,
 Chelingsong-Popov R., Weber J.N.;
 RT "HIV-1 gagD/envG recombinants in Russia."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF051469; AAD02596.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 FT NON_TER 1 90
 FT NON_TER 1 90
 SQ SEQUENCE 90 AA; 9755 MW; 6F04439DFE45B5EB CRC64;

Query Match 70.8%; Score 34; DB 12; Length 90;
 Best Local Similarity 55.6%; Pred. No. 12;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGE 10
 ||:|:|:
 Db 61 QNVTTRIGE 69

RESULT 12
 O51393 PRELIMINARY; PRT; 391 AA.

AC O51393; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE ALGJ (ALGINATE O-ACETYLTRANSFERASE ALGJ).
 GN ALGJ OR PA3549.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OX Pseudomonas.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Franklin M.J., Ohman D.E.,
 J. Bacteriol. 178:0-0(0).
 RL [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Storer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL: U50202; AAB09782.1; -.
 DR EMBL: AE004775; AAG06937.1; -.
 KW Transferrase: Complete proteome.
 SQ SEQUENCE 391 AA; 43106 MW; AE048823947D5503 CRC64;

Query Match 70.8%; Score 34; DB 2; Length 391;
 Best Local Similarity 60.0%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 QNTTARIGE 10
 ||| |::||
 Db 222 AONFVTRVGE 231

RESULT 13

ID Q9ZIC1 PRELIMINARY; PRT; 401 AA.
 AC Q9ZIC1;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE EXOEXORIBONUCLEASE VII LARGE SUBUNIT (FRAGMENT).
 GN XSEA.
 OS *Pseudomonas fluorescens*.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC *Pseudomonas*.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MF0;
 RA Regard C., Meriau A., Leriche F., Guespin-Michel J.;
 RT "Genetic studies of thermoregulated genes in the psychrotrophic
 RT bacterium *Pseudomonas fluorescens*: unexpected role of exonuclease
 RT VII.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF033853; AAC77362.1; -.
 DR InterPro: IPR003753; Exonuc_VII_L.
 DR Pfam: PF02601; Exonuc_VII_L; 1.
 FT NON_TER 1
 SQ SEQUENCE 401 AA; 44453 MW; 882B6EFA69BDB31 CRC64;

Query Match 70.8%; Score 34; DB 2; Length 401;
 Best Local Similarity 66.7%; Pred. No. 63;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTTARIGE 10
 |::|::|
 Db 372 QRLTARLGE 380

RESULT 14

ID O91900 PRELIMINARY; PRT; 459 AA.
 AC O91900;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CN30.5;
 RA Moriyama H.;
 RT "HIV-1 in Congo."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF056186; AAC61999.1; -.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW Envelope protein.
 FT NON_TER 459
 SQ SEQUENCE 459 AA; 51218 MW; 123C315B3419500C CRC64;

Query Match 70.8%; Score 34; DB 12; Length 459;
 Best Local Similarity 55.6%; Pred. No. 74;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTTARIGE 10
 ||::|::|
 Db 337 QNVSAKIGE 345

RESULT 15

ID O30965 PRELIMINARY; PRT; 715 AA.
 AC O30965;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE METHYL ACCEPTING CHEMOTAXIS PROTEIN.
 GN MCP-1.
 OS *Rhizobium leguminosarum*.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yost C.K., Rochepeau P., Hynes M.F.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF022807; AAC46418.1; -.
 DR HSP: P02942; 1QV7.
 DR InterPro: IPR000122; Chemotaxis_transducer.
 DR InterPro: IPR000658; DUF5.
 DR InterPro: IPR003660; HAMF.
 DR Pfam: PF00672; DUF5; 1.
 DR Pfam: PF00015; MCPsignal; 1.
 DR SMART: SM00304; HAMF; 1.
 DR SMART: SM00283; MCP; 1.
 SQ SEQUENCE 715 AA; 76671 MW; CBD74CA16DA0DF81 CRC64;

Query Match 70.8%; Score 34; DB 2; Length 715;
 Best Local Similarity 66.7%; Pred. No. 1,2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTTARIGE 10
 ||| |::|
 Db 235 QNTTARLGD 243

Search completed: April 24, 2002, 09:20:14
 Job time: 243 sec
